

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGT**CATG**GCGTCCCCGCTCTCGGAGAC
 TGCAGACTAAACCAGTCATTACTTGTTC AAGAGCGTTCTGCTAATCTACACTTTTATTTTC
 TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
 TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
 AAACCTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACCTGGTCGCTGCCATCGTAGG
 ATTTGTTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTTGAAGC
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
 TGTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
 TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
 ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
 ATTTCCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCCTCTCG
 TGCCATAACAAATAACCAGTATGAGATAGT**TAA**CCCAATGTATCTGTGGGCCATTCTCTCT
 CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
 ACAACACTACTTACTGATAGACCAAAAACTACACCACTAGGTTGATTCAATCAAGATGTAT
 GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTGTTAGATCG
 TTGAAACCCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLENEKATNVFP
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDINYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCAAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGTTGGGCCCGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGCTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGTAGGCTCTGGAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCAGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAGAGGGT
 GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGTTCGCCCTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAACTGAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGAACAGATGACAGTGTGACACCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGAATCTTGTAGATAAGTAAATATCTGACTCACGGTCACCTCCAGTGAAT
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTGATGTTTTTGTCTGCTGTCATCTACTTTGTCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAACACGATAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPFRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

Downloaded from www.physiology.org/journal/ajpcell by \$\${user} on 05/02/2015. Copyright © 2015 American Physiological Society. All rights reserved.

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTCAGCCATTG GCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACG GACTG
CAAG**ATG**GAGGAAGGCGGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTCAGAAATGAAAAAA
AAAAAAAAA

FIGURE 6

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGNNLGGLIKMHVLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPPYFHISM
GCAFINLNCILASQHAWAQLTFWEASQLYLLFLSLTLATVNNARWLEPRTTAAMWALQTVKEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTTCAGATTTTAAAGCCCATTTCTGCGAGTGAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTTGATTATACAAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACCTTGGCAGCCAGAAGCTTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTAAGTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTTCGGCGTGTGGCTCCCAGTACTGAGTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACATAAAATATGCTTCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAATATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCCTCATGCAATTGAACCAGGATTGTTCAAAACAACTTTGGCAGATCCAGTAAAGGTAATTTGAAAAAAAACCTGCCATTTGGGAGCAGCTGTCTCCAAGCATCAAAACAATATGGAGAAGGTTACATTTAAAAAAGTCTAGACAAAACCTGAAAGGCCAAATAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAAATCTCTTCCCTAAGACTCATTATGCCGCTGGAAGAAAGATGCCAAAATTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTTGTTGAAACAGAAAGCAGAGCTGGCTAATCCCAAGGCAGTGTGAAGTCTCAGCTAACCAAAATGTCTCCTCCAGGCTATGAAATTTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGAGTCAATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTGCTCAAGTCTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCCTGCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATCTCAAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCAATTTACAGTAACCTTGTGAATGTTAAGTATCATCTCTTATCTAAATATTAAGAGATAAGTCAACCCAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEIPEGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTACGGCGCTGCC**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCTTTGGGCGCTCGCCACCACCT
 GTAGTCATGTATCCACCGCCGCCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGCGGGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTCTGCAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAATTGCTGGGTTAAACACGCAAAATCCACCCGCTCTTACCAG
 CTCCTCAGAAGGGGACACCCAGCCTGAGAACTTACCTGAGATTTCGTACACAGAAGACAA
 AGACACATCCAGCGGGGACCCTCACCTGCAGATTAGACCCCAAGCCAAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCCTGTGGATCCCCGCCCGGAAGGAG
 ATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCACTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTCTTCTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCCTCGGTCTCAGCTGATCGACGCGCTGGACACCATTGTGGATCTTGGGTCT
 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGAGCG
 TGGAGTCAACCTGTTTGAGAGCAGCATCCGATCTCGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCCTGC
 CTTCAGAACACCATCAAGAGATTCTTACTCGGATGTGAACATCTGGAGTTGACCTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTACGTGGAGTTCGGG
 GAGCTCTCCGCTCTCACAGGGGATAAGAAGTTTCAAGGAGCAGTGGAGAAGGTGACACAGCA
 CATCCACGGCGCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTCAACCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACACTACGTGGA
 AGCCATCGAGGGTGTGAGAAGCGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG
 TGGGGGAGCTTGCCCCACGGCCGCTTCACTGCCAAGATGGACCACCTGGTGTGCTTCTTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCTGCCCGCCAGCCACATGGAGCTGGGCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCATTCAACCTTTACCCCCAGCCGGGCCGTCGGGACGTGGAGGTCAAGCCAGCACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCCGCTCACAGGGGA
 CCGCAAATACCAAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCTTACGTGTTCAACACCGAAGCCCCACCTCTGCCTATCT
 GGACCTCGCT**TAG**GGTGGATGGCTGCTGCTGGTGGGGACTTCGGGTGGGCGAGAGGCACCTTG
 CTGGGTCTGTGCAATTTTCCAAGGGCCACGTAGCACCGGCAACCGGCAAGTGGCCACGGCT
 CTGAACCTGGCTCTGGGCTCCTCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GCGCGTCACTTGTGTGTGATGCGGGGTGGGCTGGGCGGCTGGAGCCTCCGCTGCTTCTCTC
 CAGAAGACCAAGATCATGACTACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
 GAGGGGGCTTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGGACAGCCAGGCTGCGAGC
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGCTCTGGAGGGGCTGCCGTGA
 CTCACAGAGCCTGAGGCTCCAGGGCTGGCTCTGCTGTTTACAAGCTGGACTCAGGGATCCTC
 CTGGAGCCGCCGACGGGGCTTGGAGGCTGGACGGCAAGTCGCTAGCTCAGTCCAGGGCCCCCT
 CCAGTGAATGGGTCTTTTCGGTGAGATAAAAGTTGATTGCTCTAACCGCAA

FIGURE 10

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSTFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLSEEQMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGQTQEEAT
KRQEAPVDPRPEGDQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSVDNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAWEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGRADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGLAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGCTCTCCACCTGTTCTGTTGGC
 CTGCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCGAGAG
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCTGTCGCCACATGCGCCGCTTCTCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTACGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
 CCTTCCACGTGGCTTCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
 ATCTGTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
 GCCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG
 AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
 AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
 GTGCTTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGCTGTGTCTGTCCG
 GGACCCCCCTGCCTTCTGTCTCACCTACTCTGACCTCCTTCACGTGCCAGGCTGTGGG
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCAGGCTGTGGG
 AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVFPRERFEELLVFPVPMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFELESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDEDFYRRIKAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTATTAAAGAAATGTTCCCTTCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT
AAATATGTCCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

GGGACCATGCGGGCGGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGACGGGACAAAG
GAGCATGTTCCGCGCGGGGAAGGCCGCTCTCCGCGGCCCATTAAGGCTCCGGTCCGCGCTGG
GCCGCGCCGCGCTCTTCCGCCCGCGGGCTCCGGGGCGGCCCGCTAGGCCAGTCGCGCCGCG
CTCGCCCCGAGGCGCCCGGCCGAGCATGGAGCCACCCGGACGCGCGGGCGGGCGCGCGCA
GCCGCGCGTGTGTGCTCCGCTCTCGCTGTAGCGCTGTCTCGCGCTGCTGGGAGGGCGCGCG
CGCGCGCGCGCGCGGCTGCCCGCGCGCTCGAAGCAGTATGGCGCGCCCGAGGGGCTGGC
AGGGCGGGCGGGCGCGCGCGAGGGCAAGGTTGGTGTGCAGCAGCCTGGAATCTCGCGCAGGTCT
GCCCCAGATACCTTCGCCAACCCGACGGTCACCCCTGATTCTAGTAAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCCTTGAAGAAATTGGACCTCCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTTCTCGGGACATGTCAATCTCTAAAGAAATTTGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCAGAGATCAACCAATCTGGTT
GGCTAAACCTTTCCGGGAATTTGTTTTCTTATTATCTCAAGGAACCTTTTGATTATCTTGGC
TCATTACGGTCTTTTGAAGTTCTCAGACTAGTATGTTTGTGTGACTGTAACTACTGTGGAT
GCATCGCTGGGTAAAGGAAGAACAATCAGCGTACGGATACCAAGTGTGTTATCTCTAAGT
CACTCGAGGCCCAACCACTCACAGGCGTGAAGCAGGAGCTGTTGCATGTGCAGGCCCTCGCTT
GAATTTCCGCTCTTTCTCATCATCTCCATCTCATCCGCAAGTTGTGTTGAAGGAGACAGCT
TCCTTTCCAGTGATGGCTTCATATATGATCAGGACATCGAAGTGTGGTATCAGGATG
GGAGAATAGTTGAACCGATGAATCGCAAGTATTTTTGTTGAAAAGAACATGATTTCAACA
TGCTCTCTGATTTGCAAGTGCCCTAACCAATTTCTAATATTTCAGGCTGGATCTACTGGAATG
GGGCTGTCAATGTCCAGAACCAAGCTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACCAAAAGGTGACTTCAGATGG
CCCGAACAATTCGAGGCACTTCTCGATATCTGCAGTGTACGCGGAACCCCATGGCAGTGG
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGTGGCT
TTTGGGCAAGATGATGATTTATTTCTCGCTGTCAAGTATCGAATAGTGCATAGAGTTCTTTAT
ATGTTTAATCAGATGGCCCTCAATCTTACCAATGCCGTGGCAACGCTGCAGACTTACTGGC
TTACACTGTGGAAGCAGGCAACTTTTCTGACAAAATGATGTTATATTTGTGGCGAAGATGA
TTGAAAAATTTTGGAAAGTTTACCAAGGAAAAAATCAAAGAGCTAGGTGACGCTGATGGTT
GACATTTGCAAGTAAACATCATGTTGGTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
TAAAGGCTCGAGTAGGATGTGCAAGTGTCTTCAGGCGATGTCTACCTACCGGCTAGCCGGTG
GAGCTCAGGTTTATTCACATATTCACCAATATTTGCTTGAAGCTTATGTCATCAAGTCT
ACTGGCTTACGGGAGATGACCTGTACCGTGTTCCAGAAAAGTGGCAGCCTCTGATCGTACAGG
CAATTTCCGATTATATGGAGCGCGGATCAGAGGGAACCTGGATTAAGCAGCTGAGCTTTAAGT
GCAATGTTTCAATACGATTTTCGAGTCTGGCACTAAAGTATGTTAGCTCTGCAATCATTT
AAGACTATTTACAGTTAAATTAGAATGCTCCAATGTCTCGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTTGCGAGGAAGATAGTATTATTGCTTTTGGTACTGTTTAAAGAAACTA
ACCGAAGAACTGCACTATTACGATTTCAAGGGCCTAGGCATTTTGGCTTTGATTCCTTT
CTTCACATAAAAAATACGAAATTACATTTTATAACTCGAGTGGTAAATTAATGCAAAATACT
ATTTGTTACATGTAAAAAATTTATTGACTTAAAGTTTATTTATTTGTTTATTTTGTCTCT
GATTTTAAAGCAATAAGATGTTTTCATGGGCCCTTAAAGTATCATGAGCCTTTGGCACTGC
GCTCGCAAGGCTTAGTGGGAAGCTCAACCTTGACAGCAGGTGTTTAAATCAAGCAAGCTGAT
ATCAAAAATTTTGGCAAGAACCAAAATTTGTCATATATCTTTTAAAGAAAGTAAATTTCA
TTGAAGCAAGCAAAATGAAGCATTTTTTACTGATTTTAAATTTGGTGCTTTAGATATATTT
GACTACACTGATTTGAAGCAAAATAGAGGAGGCACAATCCGACCACTTAATGGAACACATTT
TTTTTCACTTAGTTTCTGTGGGCAATGTGTAATTTGATTTCTCGCGTTTAAATCTCAGAG
TACTTTATTTCTGTCTGTCTCCCTCAATTAAGTATCAAAAACAATATTCAGTCATTTTAAATGGC
TGCAATAAATCACTGCAACAGGTTTAAATGTTCTGTGTTAGTGTGAGCACTCAATAAATA
TTGAATGAATGAACGAAAAAATAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDPTLPNRTVTLLISNNKISELKNGSFSGLSLLERLDRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQ
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMP
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGFWRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
 DERVWLWAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRITGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGTCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVGLSVLLTAATVAGVHVKQQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

Index

FIGURE 19

CTGTCGCTTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT
 CAAGTGTGGCTTAATCCGCTCCACCACCAGATCTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACAAACCACCACGACGTCATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCCTTCTGCTTCTCCGTGACCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCGGCCCGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCACTCAGCGGCATCGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTCCCCAGCTTCCGTGCGGGCTGGCCCTTGCTGTC
 TGTCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCTCTACAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCCTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCACCTTTTCTTTCTCTTCC
 CAATTCTTGACTCTAACAGTTCTTGGATGCATCTTCTTCCCTTCCCTTCTCTGTGT
 TTCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTGCGGCTTCTTATCGCCTGT
 TTTGCAAGCACCTTCTCTGTGCTTGGGAGCCTGAGACTTCTTCTCTCCTTGCCCTCA
 CCCACCTCCAAGGTGCTGAGCTCACATCCACACCCTTGACGCGCTCCATGCCACAGCCCC
 CCAAGGGGCCCATTGCCAAAGCATGCCGCCCACCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTTAAATTAATAAACATATATATATATAT
 ATTTGGAGGTGAGTAATTTCCAATGGCGGGAGGCATTAAGCACCAGCCTGGGTCCCTAGG
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAVTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCS
 LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSPSDSPAALSAFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSELDGLLGS PARLASQLLGDE
 LLLAKLPSPRESAFRSLGLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
GGCACCCTCCTGCTCAGTGCACATTTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCTTTACAGACAGGACAACCTGTGATATTTAGTTCTCTGATTTGTAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG
AAGCCTAC**AATG**TTGGCCTTAGCCAAAATCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGAAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAATTT
TTAAACCAATGAAAAATAACCTATTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAAATAAACCCCTCAAATCTCAAGGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCGAGTCAA
AACCACATCTACCATTTCACAAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCTT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGCTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCCTATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATCAAAACTCTTTCCAA
ATACGTGAGATCCCCAAAAAGAAAATAGAAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTGTGGGCTACTTGTGTGTGAAAAAGGAAAAC
GGATTCAATTTCCCATCGGCGACTTTATGACGACAGAAAATGAACAGTTCTGCGATTAGACA
ATGCAACCGGAACCTTATGATGTGAGTTTTGGGAATTTAGCTACTACAATCCAACCTTGAAT
GATTACGCCATGCCAGAAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
CATCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGATTTTGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
TCACCTATTACGCCCTGCCTCATAACTAAATAATAAAAATTTATCCACCAAAAAATCTAAA
ACAAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCACGGGGCCATGGCAGGAAAGCTGACCTACCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAGGTTTTGGGAATTTAACTTGCTTAAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFNNKSLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGILLCGKRKTDTSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNP TLNSA
MPSEENARDGIPMD DIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**TATG**TGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCITTTCACTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGCATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTG⁺CAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCCTTACCTGGACTTGTGTCTGGGGA⁺ACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCCAAACTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAA
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC
 GTTGTTTTTTTTGTGTTGTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTGTTTTGAACTTTTTGTGTA⁺AAATATA
 TCAGATCTCAACATTGTTGGTTCTTTTGTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTGCAGTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA
 CCCTATAATAAATTTTACTCTATACAAAAA⁺AAAAAAAAAAAAA

FIGURE 26

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDDPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNRKSFRLRRRDLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACACGAGCAGCGACTCTCT
CTTCCAGCCCAGGTGCCCCCACTCTCGTCCATTGGCGGGAGCACCAGTCCTGTACGCC
AAGGAACTGGTCTTGGGGGCACCA**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGTAGTGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCGAGCCTCC
CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAAACCTGGGG
GGCCCATACCCCCACCAACTTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCCGGGTCA
TCACCCGGCAGAAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGGCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCC
CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACCCAGGAAGTCCA
GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
AGGGGGCTGTGGTGGCCGGTGAAGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG
GAAGCCAGGGACCAGTGGGTCCCCCGAAAGCCCTGTGCTTGACAGAGTGTCCACCCAG
TGCT**TAA**CAGTCTCCCGGGCTGCCAGCCCTGACTGTGGGCCCCCAAGTGGTCACTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
ACAGTCCCTGACAAAGTGAAGGAGGGCAGCTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACACTTTTAAAAACA
GCTACAGGGTAAATCCTGCAGCACCCACTCTGGAATAACTGCTCTTAATTTTCTGAAGG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGCATTAAATCCTC
TCAAGCGCTCTCAAGCACCCCGGCCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGTGG
GATCAGGTTGAATGAATGAACTCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAAGGGACCTCACCCCTGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
TGTCACAAATATTCTGCAGTCTCGACAGGGAGCCTGGGCTCCGTCTCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
CCAGTGCTGAGATATAATGCACAGCACAAATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA
AAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGI VDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVFVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSILLAQEAQGPGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATC
 AAGTTCAGGGGGCCCCCTGGCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
 TGGGAGACGCCCTTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGCCAAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATAACCCGGAACCTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAACTTTGGGACCAACAC
 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCACTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA
 TCCAGACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGACATAAACCC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGAGCGGGGAATCTGGGATTAGGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGA
 GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTAACTTTGACACTTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
 AGCTCTCGCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
 CCCTCCTTAAACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAATAAACCTTA
 GCTGCCCCACAA
 AA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPHGSHGAWETSGGGHIGFSQGGGLGGQGGQNPGGGLTPVWHGYPCNSAGSFGM
NPQGAPWQGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNRYRQGSSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTCTGGATGTGCGGAATCTGCTGCAGCAGAGGGCTGCAGGCCCGCGGGCGGTCTCACC
 TGCCCTGGCTGGTGGAGTTTCTCTCCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTCGCGCTGCACCGGGAGCTTGGTGTGTCGAGGAGAGTGAGGGGAATGTTGTTTCTGGAACAAAGC
 TGTGCTACTTGTGCTCCTGGGCTGGCTTTTCAGATTCCCAAGCTCCCTGAGGACTTGTCTTTCTGGAAGAGG
 GTCCCTCATATGCCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGGCCCTGTGGGTGGACCAAGC
 AGCTGCTCTACACCTGCTGCCCTTACATCGAGAGACTCCGGAAATGCTCGCTTCGTGGGTGTGAGGCAGTAGTG
 GACGGAGTGGGGGCTTCACTGAGGAAATACCCCCACACTACCACAGCTGGGAGCCAGCCCTCCACAGACA
 CGCAGGGCTGCAGGCACAGCTCGCCACAGCCCTTTTCCAAACAGCAGCCGCTCTCTGCGCCGAGCCGTAGAGT
 TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAACATCAAGGCTACATCTGGTGGCAGATCTGGTGGCCGAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCAGGCCAGCTGTTGGAGATCT
 TGTGTTCCCGAGCTGCGCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAAGCCGTTCTGAGCAGTGCAGAGAACATTTGCTGTGGGG
 TTGCAACAGAGAAGCCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCAGGCCAGGGTCTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAC
 GTGCTCTCCTTGGCCCTGGGGCCACGGGACCTGACAGGGAGTCTCCCCAGAGCATCTGGAAACAGCTCTTAGGC
 CAGCTGGGCGAGAGCTGCGGTGCCGCCAGTTCTGTGCCAAGCTGCTGAGCAGCATCTGGCAAGTGTGCTGTGTG
 GAGTTAGCTTCCCTCCTCGTTCGAGATCAAAATTCCTATCTAGGGCCCGGGCAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTTCGACATCTGCTTTCTTGTGGAAGGAAGACTTTCAGGGGCCGCTCCGCTGCAGCTG
 CTGCTGACGGGCAAAATGTGGGCTTCTGGCAGACAGGGCAAGGGAGTGGGACTTGTCTGCTATTCTTGTCTA
 CGGAGCTGGTGGAGAGGGCTGTGATGGGCGGATGGAGATAGAGGAGCTGCTGGCAGCTCTCACCAAGGCCAG
 TGCCAGGGGACTTCTCGAAGAAATAGCAACACTGCTAATCTGTTCTAGGCCAGGCCCACTCCAGAACCC
 CAGCTAAGAGCTCTGAGTTGGTGCAGCCAAACCGGSGCACTGTCTGGCCAGAGCTAGGCTGAGAAGTGGCC
 CTGCTTGGGCACTGCACAGAACCTTGGACCCCGGCTCACGAGGAGGCCAAGTGCCCAATGCAGACCTCAC
 TGGTTGGGCTGTAGCTGGCTCTCAGTCAGACTTCTGCTCTAAGGGGTGTCACTGCTGGGCACTCCACACAGCGA
 ATCCTAGAGGAAGAGAGTTGGCTGATTTGGGATTAATGGCAGAAAGTCCAGAGATGCCAGTCTGAGGTAGAGA
 GAGGTGGTGTGTTGTTATCTCTTGGATACTAAATGAAATGAGGTGTGGGGCTTGTCAACACAGAAATCGAGGCT
 CATTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGGAAATTCATGACAGAGGCAAAATGACTCTCTGCTTAAC
 TTAGAAGAAAGTTAAACATGAATCTGGGAGTCAACATTTCTTATCACAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCATAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAGGTGCGGG
 GACTGCCCTGAGGTGAGGAATTAAGACCAAGCTGGCCAACTGGCAAAACCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGAGTGAAGCCGAGGTGCAACCACTGCATCCAGTCTGGGTAAACAGCCGAGACTTCTAG
 AAAAAAGCTTAACAAACAGATAAGGTAGGACTCAACCAACTGAACCTGACTTTCGCCCTGTACCTTCAGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCAGAGGCAATTTAGAGCTTTTGAATAAA
 CTGGTTTCTTTAAAAAAGGGCTTTTATTAAAAATCTCCCAACAGATGGCTCCTGCAATTCGCCACAGCTG
 TGGGCGGTGCTCTGAGGAAAGGCCCTGTTTCCCTGAGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
 GCGGTGCTTGGCGGCTTGGCGTGTGTCTAGCTGCTTCTGCGGGCACAGAGTGTGCGGGGTCTGGGGGCAACCGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGTGGAGGCTGTCTTAAACCAGACCTTGAGGTGCTCCTGAGATGCTG
 GGTCCACCTGTGAGTGGCAGCGGGAGCAGCTGTGGCGGTGCTCCTCTCTAGGCACTCCTGGGGAACCTAAGCTC
 GGGCCCTCTTTTGAAGAGCCGAGGATGGGGTGGGTGTGGGGGACTCAGGGGAATGGCTGAGGAGCTACGTGT
 GAAGAGGGCGCGGTGTTGTTGGCTGCAGCGGCTGGAGCGCTCTCTCCTGAGCCTCAGTTCCCTTCCGTTCTA
 ATGAAGAACTGCGCTCTCGGTGTCTAGGCTATTAGGACTTGGCTCAGGAAGTGGCTTGGAGCAGCGTCA
 GTTATTTTTCAAACTGCTCGCAGCTTGGCTGAGCAGCTCATGGAATGGCCATGTCCCTCTGCTGGGTGGAC
 GTGCGGCTCGGAGTGTGCGAGCGAGGGCGGGGCGAGAGCTGCGCTGGGGGTGAGGGGAGGCGCCCGGAGAGG
 CCTCAGAGAGTGTGGCTCCGCAACCAAGCAGGAGGGCGGGCTCCCGCGCCAGCCGCGCCAGCTGTCAGG
 GGCCGGTAGCAAAATGGAGTGCAGCTGGGTGCTGCGCAGCAGGTAGCCCTTGATGAGTGCAGGAGCGG
 TCGTCCGCGAGCTGGAAGCAGCGCCGCTCCACACACAGCAACAGCCGCTGCGCT

FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAGLATEKACAWLSANITAL
 IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

CCCTTGCACAGGCTCTCTGTGGCTGGTTCTGGGGGCTCTACTGAAGGCTGTCCTTGATCAGGAACCTCG
AAGACTCTCTGCTGTTTGGCCACAGAGTCTCTGACGTTCTCTGAGGTGTGAACCCACATCTCC
TGCCCCAGGGCCACCTGTCAGAGCGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATCC
AGTAGCAACAAAGAGCAGCGGCTGACAGGTTCTGTGATCTCTTGTGCCCTCATCACCATTCT
CATCTCTACAGCTCCAACAGTGCCAATGAGGTTCTTCATTACGGCTCCCTGCGGGGCGGTGA
GCGCGCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTGTCGGG
AACAAGACATGCCCTCTCGGTGCCAACAGTGTGTGATTGTGTCAGAGCTCAGCCACCTGCG
GGGACCAAGCTGGGCCCTGAGATCAGCGGGGCTGAGTGTACAATTCCGATGAATGATGAC
CCACCATTGGCTACTCATGCTGATGTGGGCAACAAGACCATTACCGGCTCTGTGGCCATTCC
AGTGTGTTCCGGTGCTGAGGAGGCCCCAGGAGTTTGCAACCGGACCCCTGAAACCGTGTTC
CATCTCTGCGGGGCCCCGAGCAAGATGTCAGAAGCCACGGGACGCTCTGTGCGCTGTATCC
AGCCAGCGGGCTGTGTTGTTCCCCAACATGGGAAGCATATGCCCTCTCTCCCGGCCGATCGGG
CAATTTGACACCTCTCTCCGGGGTGAGCGGGGAAGCAGGAGGAAGTCTCATCTGTGTT
GAGCACAGGCTGGTTTACCATTGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
GCATGTGCCCCCACAATCTACTGCAAGTCAGCGGCCGCCGCTCAGCGGCATGCCCTACCACATAC
TACGAGTCCCAAGGGGCGGAGCAAGTGTGTCACTACATCCAGAATGAGCACAGTCCGCAAGGG
CAACCACACCGCTTTCATCCAGGAGAAAAGGGTCTTCTCATCTGTGGGCCAGCTGTATGGCA
TCACTTCTCCACCCTCTCTGGACCTAGGCCACCACCGCTGTGGGACCTCAGGAGGGTCAG
AGGAAAGGACGCTCCGCCCCAGCGCTCAGGCCAGGGACCATCTTGTCGCCAATCAAGGCTTC
CTGGAGATGTCCTCCGAGCAATCAGGCGCTTGAGGAGGATGTATCTCCAGGCAATCAGGGCC
TGGGAATCTGTGTTGGCGAATCAGGAAATTTGGGAGTCTATGTGTTAATCAGGGGTGTCTTTC
TTGTGCAGTCAAGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCAGTGCATCATCTG
AGGCTAAGGACATGTCTCTTCCATATAGGGCTTGGTTGAGAGCCCGAGGAATGAGCCCCCA
ATCACTCCCCACTCTGCTGGGATATGGGCTCTGTCCCAAGAGCTGGGAATCTGGTGTGTG
CCCCCTCAATTTCCAGACAGCAAGAAAGAGATTTGTGGGGGTAGAAGCTGTCTGGAGGCC
GGCCAGAGAATTTGTGGGTTGTGGAGTTGTGGGGCGGTGGGAGGCTCCGAGAGGTGGGA
GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAAACCTTCCCCCTCTCTGG
CACCTCTCTGCCACACAGGTTTCCAGTGGCGGAGTCTGAGACCTTCTACCTCCCCATCAA
GTGCGCTCGGGTCTGTCTCCCCCTTGACCTCCCGACCTATCCCTTGTGCGAAGCT
CAGCTTCTTGGGGGGTCTGGGTGACTCTCCCACTCTGAAAACTTTAGGGTATTTTGTG
GCAAACTCTCTCAGGTTGTGGGGAATCTGAAGGAACGGGACAAAACCTTAAGCTGTTTTCT
TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCAGGCCTCCTTTTCTGCCCT
CTAGCAGGAGGTTTCTTCCAATGTGTGGAGGCGCTTGTGGGCTGCCCTTTGTCTGGAGTCA
CTGGGGCTCTCGAGGTTCTCCCTGCACCTCTGTGCTGTGGAATGGCTCTCGGAGCTGT
ATCACTCTGGGTTGTGCTCCCTGGCTCTGTATCAGGCACCTTTAATAAGCTGGGCTCAGTGG
GGTGTGTTGCTCTCTGCTCTCTTGAGGCTGGAAGGAAAGGCTCTCAGGAGGAGGCTGTGA
GGCTGGAGGGACAGATGTAGGAGGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
GGGCGGTGACTGCCCCAGACTTGGTTTGTAAATGATTGTGACAGGAATAAACACACTACGC
TCCGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSADVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFRVLRPQEFVNRTPETVFIFWGPSPKMQKPQGS�VRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPLQRMPYH
 YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTGTGGCGTCTTCTAAAGGAAAACTAAATGAGGAATCAGCGGACGGGAGCGAGCGAGCTT
 GAGGGAAGCATCCCTAGCTGTGTGGCGAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGCTCTGAGGGGCTTG
 GGCAAAGGTGAAAGAGTTTCAAGAACAGCTTCTGGAACCATGACCCATGAAGTCTTGTGCAGATTATACCGT
 CTGAGGTTAGCAGCTCGAACTTAGAAGAAGTGGAGTGTGCCAGGAGCGGCGATATCTCTTTGTGTGACCTGGC
 GGCTATGGGAGCTTGGCTTCAGACCTTTGTGATACACATGCTGCTGGGAGCATGACGGCGTGGAGAGAAAT
 AGGCGTTGAGGTCACACTGGCTTGGCTCCTCCTTAGCCACAGCAGGCTGCTTTGTGACTTTGAACAGAGTCCCTCAG
 TCCACCGTCCAGGCTGCGTCCACCGTCCAGAAGCCGGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA
 AGGATGAATGTAACTGGCGCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCAACC
 CAGGGAGCCCTCGTCATCATCTGCCCTTAAACAACACACTGTGGGACGGTACAGTGTGTGGCCGGGATGCCGTGG
 GGGCTGTGGCCAGCGTGGCCACCTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCAGTGTG
 ATTGAAGTGGATGAGGGAACACAGCAGTCAATGCTGCCACCTGCCTGACAGCCACCCCAAGCCAGGTCGGG
 TAGCGCTCAAAACAAGATGGCTGGAGGCCCTCCAGAGGTAACTACCTGATCATGCGCTCAGGGAACCTCCAGATT
 TCGAGTCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTCAAAACCATGACCCAGGAAGTGAAGAAC
 TCGGCTCCAGCGCAGGCTAGGTTGTGGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC
 CAAACCATCATCTGCACAAAGGCCAGAGTCTCATTTGAGAGTGTGTGGCCAGTGGAAATCCCCCCCCAGGCGCT
 ACTTGGCCCAAGATGGGTCAGGTGTCAACCGCTCACAACAAGACGGCGCTTCTGCTGAGCAACCTCCTCATGTAC
 AACCAACCGAGGAGACTCAGGCACTACCCCTGCATGSCCGCAATGGGGTTGGGCGAGCCGGGAGCGGCTGCT
 ATCTCTACAATGTCCAGTGTTCACACCTCTGAGCTACCATGAGCTATCCAGCTGTGCTATCCCTGGGG
 CAGAGTCCCAAGCTTACCTGTGAGTGGCTGGAACCCCGCGCTGCTGCTGAGTAATGCTGTGCC
 CTCTATCCAGCCAGCGCTCCGGCTCTCCCGAGGCGCTTGCCTGCTCAGCATGGGGCTGAGGACGAAGGC
 GTTACCACTGCATGGCCAGAAACAGGTTGGGAGCGCCATCGCTGATCGACGCTGGGACCTCCAGGCCAAGC
 ATAAACCCCAAGGCTTAGGCGAGTGTGAGCTGGCTACTGGCACCCTCTGTATACCCCTCAAATCGGGACAC
 CTTGAGCAGACTGTAGGCGGCAACCGGCGCTCCCAAGCCCAACGTCGTGGGGCTGCTTTCCCGAAGTGT
 CCAGGAGAGAAGGGGAGGGGGCTCCCGCGAGGCTCCCATCTCTCAGCTCGCCCGGCACTCCAAGACAGAC
 TCTATGTAACTGGTGTGGCGCTCGCATGAGGCGAGTGGCGGCGGCAATCCTCTACTATGTGTGCAAAACAC
 CGCAAGCAGGTCACAAATTCCTCTGACGATTGACCATCTCTGGCATTCCAGCCAAACAGCAGCGCTGACCTCT
 ACCAGCTTGAACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAATGTGGGGAGAGGGCCAGACAGCC
 ATGCTCACTTCCGAAGTGGAGCGGCGCCCAAACCGAGATCATGGCCAGCAAGAGCAGAGATCCAGAGAGAC
 GACCTGGAGCGAGTCCCGAGAGCAGCAGCCAGCCAGCAACCGGCGCTCTCCCCCGAAGCTCCCGGACAGG
 CCCACCATCTCCAGCGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCCGGGAATGGTGGGTCCCACATC
 CAGTCTCTCCGTGTGAGTACAGAGACTAAGAAGTGGGAGCATGGATTCTGGCCACCGAGCGCATCCCCCA
 TCCCGCTCTCCGTGAGATCAGCGGCTTAGAAGGCACTCTCATAGTTTTCAGTCCGGCTGTGACATG
 CTGGGGAGAGCGAGCCAGCGGCCCTCTCGGCCCTACGTTGTTGCGGCTACAGCGTCCGCTGTACGAGG
 CCGTGGCAGGTCTTATATCACTTCAACGATCGGCTCAATGAGACCACTCATGCTCAAGTGTATGTACATC
 CCAGCAAGTAACAACACACCCCAATCCATGGCTTTTATATCTATTATCGAACCCAGACAGTGAATATGATAGT
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCGCTCGAGCCAGAGACCTCTCAG
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGGAGTTCAGCAACGTCGATGATCTGTGAGACCAAGCT
 CGAAGTCTTCTGGCCAGCTGGTGCACCTGCCACCCCACTCTGGCCCCACCAAGCGGCCCTTCTTGAACCC
 ATAGAGCGGCGGCTGGGCACTGGGCGCATGGTGGCTCGCTCAGCGACCTGCGCTATCTGATTGTGGGGTCTGCT
 CTGGGCTCCATCGTTCTCATCATCTCACCTTCATCCCTTCTGCTTGTGGAGGGCGTGGCTCAAGCAAAAACAT
 ACAACAGACCTGGGTTTCTCGAAGTGGCCTTCACACCTCTCGCCGTATACATGTGGTGCATTTGGGAGGACCT
 CCAGGCCAGCGGCTCCAGGACGCCCTACCTCAGTGGCATCAGTGGACCGGCGCTGTGCTAATGGATGGATCAGT
 ARTAGGGCTGCCCTCGGCTGCACTGGGCTACCCGGGCACTGAAGCCGCCAGCAGCATGCCCAAGCGAGCTTCAG
 CAGCAAGTCCACCAAGCTCTGCTGAGCGAGACCCATCTTGGACCATGATGACCCCAAGCTCAGCAGCTCAG
 CAGAGGCTCCAGGTCTAGCCCGGCGAGCGCTCTTCTTATACCACTGCTCGGACAGCTCAGCAGCTCATCAGT
 CTGACAGCCCATCAGCATGCTGTCACCAACCCAGGAGCAGCTGCTGCTGGGCGAGTCAAGGCTGAGGAGGCC
 CCGAGTGCCTGTCTCGAAGCAGGTGGGACCTCCATTTCACTCAGGCCCATCATGCTGCTGGGCTTGTG
 CCGAGTTGAAGAGGTGACAGCTGCTGACTCTGCCAAGTGAAGTGGAGGAGCTGGTGTCCCGACACCCCGTAGGG
 GCTATCTAGGACAGGAAGTCCGATCAGCTCTCCCGGGGCACTGTTGGCTGTGCTTTTGAACACCACTCT
 CTCACAAATTAGGCAGAAGCTGATATCCAGAAAGCATATATATTGTTTTTTTTTAAAAAANAAGAGAAAAA
 AGAGACAGAGAAATTTGTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTTGTAATAATGTGTA
 TATGTTTTATATTTCTGGAGAGACATAAGAGTCTCAACCGTTGAGGTTGGAGAGGGAATAAAGAAAGCTGCCA
 CCTAACAGAGGTCAACGAGAGGCCAGCATAGCTGGCAAGAGGAAGGATCCAGGACATGGTTCATCAAGAGCA
 TGAGGAGACAGCAAGGGCCGATATCAAGCCTGGAGACCCACAGACAGATGGCTGATCGGTGCTACGGGAA
 ACATTTCTCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCATATGAGCATTAAGAAAACCTTCCAGAT
 CATATATCCGTGGCAACATATCTCTAAAAACAACACTGTAACTTCAATAAATGTTTAGTCTTCCCTGTAAATA

FIGURE 36

MLRGTMTAWRGM RPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGTVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQC VARM PAGA VASVPATVTL
 ANLQDFKLDVQHVI EVDEGNTAVIACHLPESH PKAQV RYSVKQEWLEASRGNYLIMP SGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVR RSTAE AARI IYPPEAQTI IIVTKGQSL
 ILECVASGIPPPRV TWAKDGSSVT GYNKTRFLLSNLLIDT SEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCM AENEVGS AHAVVQLRTSRPSITPRLWQDAELATGT PVPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGA PAEAPI ILLSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSF RVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYYRPTDSDNDSYKKDMVEGDKYWHS ISHLQ PETS YDIKMQC FNEGGESEFSNV M
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSI VL
 IIVTFIPFCLWRAWSKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHC PGELQQQSDTSSLLRQTHLNGYD PQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPF HSG
 PPCCGLGLVPVEEVDS PDSCQVSGGDWCPQHPVGAYV GQEPGMQLSPGFLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTGCTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATGC**AGCCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCGGGGTGTCCCCAGCGCCCTACTACCCAGGCCTACTACGCCAGG
 CACCCCCAAAACCTTGACCTTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTACGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCCGATGTGTGCCTCTACTCTGAAGTTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCACCAAGTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTGG
 AAGTGCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGAAATTTATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGAGCAGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCCTGGAGGTCTCAATGCCT
 CCCCATACCTTGTTCAGGCCCTTGTGGCTGTGCCACCATCCCAACCTTCAACCCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAGCCTCACAAGCCCCCTCTCCT
 AGTTCAATTCACAAGCATATGCTGAGAATAAACATGTTACACATGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTAEETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPLGTTTGGTPKTLDLRGQAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGQAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLCNLLANVSTVADHFDHIRAVIGSEFIGGIGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFPYQGLSTSCH
SHLVPQNGHQATHLEVTQPTNRPVWRSSNASFYLVPGLVAAATIPTFTQWLK
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCACTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCCTGATGTCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAAACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTCTTCTCCTT
 CTCCCTAACITTAGAAATGTTGACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTGTCTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA
 GGAACCTAGTGTCTGGGAGGAAAGCATGGCCAGCATTACAGCATGTGTTCTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGCTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
 CACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACCTCGTTGTACCAAGTGCATGGA
 GAGAAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG
 TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHVDEAYCLLCCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

ACGGCGTCTTCGCTTGGGTTGCTCAATTTCTGTCTCTGAGGCGTGAGACTGAGTTTCATAGGGTCTTGGGTCCTCCGGA
AGGACGAGGGGTTGAGGGAACAACATCTGCAAGCCCCCGGACGACCAAGTAGGGGCGCCCGGTGTGGGGGTCCTCGG
TCCCTTTGCATTTCCCAACCTCCCGGGCTTTGGCTTTCTCTGGGGAGCCCTCCGGCGGAATGCGGGGTTCATG
CGGAGCAAGGATTCGTCTGCTGCTCTCTCTCTCTCTGCGCGGGTGCTGATGTGTGAGAGCTTCACAGATCGCGAGT
TCGCGGCGCAAACTCAACTCCTCAAGTCTCTCTCTGGCGGGGAGACGCTGGTCAAGCCGCAATGCATCTGCG
GGCATTCGCAACGAGTGGCATTCGGCGCGAGTAAAGAGGCGAAAAAGCTGGGGCGAGCCCTACCTCTTGAGCATGT
GATAAGGATGTGAAGTTGGAGGATTTGGCCAGTCCCCACAAGGATCATCGGCTGCATGGTGTGTGGGAGA
AAAAAGAGGCGCTGCCACCGGATGGCATGTGCTGCCCGGATCCCGCTGCAATTAATGGCATCTGTATCCGAGT
ACTGAAAGCATCTTAACCTCCACATCCCGGCTCTGGATGTACTCGGCACAGAGATCAAGAACCGGCTATTAC
ACAAACCATGATCTGGGATGGCGAAGTCTAGGAAGAGCCATCAAGATTAAGATGTTCACATTAAGAAGGCGATGAAGGA
GACCCCTGCTTACAGATCATCAGATCGATTGAAGGTTTTCGTGCTGCTCATTTCTGCACAAATCTCCAA
CCAGTGTCTCATCAGGGGGAAGTCTGTAAACAACCAACCAAGAAGGTTCTCATGGCTGAAATTTCCAGCGT
TGGCATGTGCGAAGGGCTGTCTTGCCAAGTATGCAAGATGCCACCTCTCCAAAGCCAGACTCCATGTG
TGTCAGAAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCAATTATG
CATGGTGGAAAAATAGGTCAGATCGAGAGGATGGCTAAAGATGAAGAACCTGATAGAATATAGATGATCACAA
AAGGGGAGCAAGAARAACATGAAGTCAGATAGGAATGGGTGACAAATCGAGTCAGCGAGCTTCTCCATTATG
CACTTGTGCTATGTAATAATATGACACATTTGTGGAATATGCTATTATTAAGACAACAAGCACACAGTGGAAAT
ACTGATGAGTACGATGTGACTTCCAAAGTTAGGTTGTGCTGGAGGAGAGGTTCCCTTCAGATTGCTGATGGC
TTATACAAATAACCTACATCGCAGATTTCTATTCAAGCTTAGAGTTTACAAACATCTCTAGTAACCTTGTGTA
TCAATAGATGCTTAAAAATAAATTGCTAAACAAGAAATGAAGAACTGAGAACTGTAATTTTACAAACAAGAAAT
TACCTTTTGATTTGCTTAACTACTCTCTGCTGTTCATCAAGAGCTTTGTGAGATAGAAAAAAATCAGCAAAAT
TCCAAATTTGCTTAAAAATTTGGCCAGCTGTGTAGGAGAGGCTTTAGGAAGACAATAAATCAATCAACAT
CCCAAAATACITTTTTTCAAATTTTAGTTTACTCTGATTAATGAAGACTGATACAAGCAAAAAACAGTTCC
TTCAGATTTCCAGGATGACGATATATCTCTTTACTCTGATGTATTCCTGCTGCTGAATGCTATTATTTCC
AACTATACCCATAAATTTGATGATGAATAAATCTTACAGACAGCAAGTAATTCACAGATGGCAAAAAAATTTAA
GATGTCCAATATGTGGGGAAGAAGACTACAGAGATCATTTTCTTAAAGTTGGCCATAACCTATATTT
GATAGAATAGATTTGTAATAATACATTTATTCATCTGCTCTGTGTAATAGAGACTTAAGCTGGATCTGACTG
CACTGGAGTAGGACAATAATTTGGGAAACCTTTTCGTTTCTGAGGTTTGGCAACACATATAGATCATATGCTG
AGGCACAAGTTGGCTGTTCACTTTTGAACCCAGGGGATGCACAGTCTAAATGAATATCTGCTATGGGATTTGTA
CATATAATTTACTATGCAAGATCAATCAGTTGAGGTCGTGCGGTACCTCAAAATATGTTTATATAG
TGCTGAGATCCTCAATATCTCAATTTCAGGAGGTTTACAAAGTGACTCTGAGTAGACAGATATGTGAGG
TTTCATTTGCCCTCTATAAGCTTTGACTAGGCCAATGGCATCCAAATTTCTTCCAAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGCGTAGTTTGGTTTCTGCGAGCATTCGGGTTAAAAAATATAAGTAGGATATGCTGTAA
ACCTCGAGTTGCTGTAATCTATGACAGACACAGTTTCTAAATTTCTGAAACCACTTACTACTTTTTTAAACT
AATCACTGATTTAAATACTTTGCTGGAGGCAAAAACAAAAAGGTTATCTTATAGCTGTGACTTTAAACTTTT
TAGACCAACAATTCATTTTGTGTTTCTTTAACTTAAATCCCATCTGCGAGCTCAAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCTGTATATCTTAAAAAATTTCAACTTCCCACTATTTACTAGATGATTAGACATTA
CTTTTCTGCGACAGGCTGCAAAACAAAAAATATAAAGTATGTCATCCAGAAGCAAAAGTTTGTATTAACAGGT
TGCTATATAGCTTTGTGAATGAAATGAACATCTCAATCAACAGTTTCTCTATTAACAATTTATCAAT
TGTGTTTCTGCAATTTTCTTATGTGCCATCTTTAAAAATATTTATTTGAAGTAAATTTATGACAGGAAT
TTAATGAGATGATTTTCTTATAGAGATCTTTACAGAAGGCTTTGACAGAAATATTTCGACGCTATGAC
TTTGTAATTTAGGAATAATGTATATAAGATAAAATCTATTAAATTTTCTCTCTCTAAAACCTGAAAAA
AAAAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

Downloaded from www.jstor.org

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCCAA
 GTGTTGGGATTACAGCGGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTGGAGAGCTTGCAACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACAGAGCCAGGCAGTCAGTGTCTCCT
 CCTGGTTTGGAGTCCTTTCCCTCCAGGCCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCTACTGTGAACAAGCTTTTGCAGCTTCCAGCAGCACCATTGAAAATATCTCTGTGCTG
 TCCACCAGCCACAGCCCAAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGCAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGCTCTCCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCATGGCTGGTGGCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAACACCAAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGCTTAAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCAAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC
 GTCTCTACTATAAAATACGAAAACTAGCCGGGTGTGTTGGCGGCGCGTGCTGTAAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEFSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**CGGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCTGCCTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCACCCGCGCTTCTGACCTGCGTGAACCGGGGACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGCTGACTGGGACCGGCAGCCGCCCGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGCGACCGCTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCGCCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCACG
 ACCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTTCTGGCGCGCCGAGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGAGTTGCTGTGGCTGCAGGGGACAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCGGGAAGGAGAACT
 GCAAAT**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCCTTGTCTACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGFDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPRGSPGNSSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKGDVNLA EFVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDLDKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGCTGGCGCAGCGGCAC**ATG**GCCGCTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACCACAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTTGAGAAGCTGCTGGACCGCCGCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATTGGAACCTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGGCCACCGGGGA
 GGACCCGTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG
 TGCCCTCCATGCTGTGCCTGGTGGCCAACTCCTGCTGTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCCTGGCCATCTTATGGTGATAACTGCAGTGGTGAA
 GGTGGACACTTCTCCTGGACCCGTGGTTTTTTTCGGGTCAACATTGTCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCTGTCTTTCGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTATTGATTCCACACACCCCTCTCC
 GCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGTCTTCTTATCACC
 AGCCTCATCTACCCCGCGCTGTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACCTTTGCTGACCTAT
 GTGGCCGGCAGCTACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGCGCTCCCAAGG
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTTCTCGTGCTCTGTAACACCAGCCCCGCT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTTACGGGCTCAAGATTGTGCCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCTCCTGGTGCACCTCATC**TAGA**AGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCA
 GTGAGCCACGTCCATGCCCATTCCTGCAAGGCAGATATTCCAGTCAATTAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCTGGCATGGTCAGTCTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCTGTGTTCT
 GCGGGTGAACAACTGCCCACTAACAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT
 GCTTCATTCCAGAGGGACAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAAGAGGATCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCTAATAAATACTTGC
 GTATTCAAAA

FIGURE 48

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYYIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKT VVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCACCAGAGAGTCA**ATG**GCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGGCTGGGGCTCAACCTGACCAAGTTACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGGCTACGCCTTGGCTCCCCAGGAAAAGGGCCACTCGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGCCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGACCGCACGATGTGCAGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCCCTAAGCTTCCGAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGCTGGCTCGTACACGTGGTTCGACGCGGCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGAGTGGCGGCATTGCAGGGGCC
 TGTCTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGCGGAGGACAGCACA
 GCCAGGTTGGCTTTGGGTACAGCCCGCGGCGCTCTGGCAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGATCTACTTTGCCGCGGAGCACACCGCCTACCCGACAGGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCGCCATCAAGATCAACAGCCGAAGGGGCGCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGACGGGCGATGTGCATGGG
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCTCCAGTCCAAGG
 CCAGTTATCTCTCAAAAACAGACCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA
 AA

FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGFHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

FIGURE 52

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFKLLFTKMLFIFN
FLFSPLPPTALICILTFGAIFLWLITRPQPVLPPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFORGLAVSDNGPCLGYRKPNQPYRWLSYQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPFAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAAFKLCVEHAYEPTPDDVAISYLPPLAHMFERIVQ
AVVYSCGARVGFQGDIRLLADDMKTLKPTLFFAVPRLNLRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLI FAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVP LACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTG DIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEK IENIYNR
SQPVLQIFVHGESLRSSSLVG VVVPD TDVLP SFAAKLG VKGSFEELCQNVVREAILEDLQKI
GKESGLKTFEQVKAI FLHPEPF SIENGLLTPTL KAKRGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

GAGGCGGAGGCCGCGCGCGAGCCGGGCCGAGCAGTGAAGGCCCTAGCGGGGCCCGAGCGGGG
CCCGGAGGCCCTTAAGCCATTCTTGAAGTCATGGGTGCGCCAGGACATTTGGTGAAGCCCAAT
CCGGTATGGACACTGGAAGCCAGGCCCTCATCAAGCCCTTTGGGGCTCGGAAGCAAGCGG
AGCTGTGTACCTTACTTGGAACTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
GACAGGGGCGGTGCTTTCTCTGTGTGACTGTCTATTGTCAATATCAAGTTGATCTCGTGGACA
CTCGCGAGGCCATCAGTGAAGCCAAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
TAGGCCGCTGGAGCCCCCAGCGGCATAGAGGCATGTGTCGCCCGCGGGTCTTGGACGTAGA
GGTGTTATTCAGTCCGACCAAGATATGTGGCAGTGGATGGCACCAGCGTGTGTGGAGGAT
AGGCCCGGGAGCGGGCGGGGCTCATCTGTCATTGTCTCAACCAAGCCAGCGGCCAGCTG
ATGGCAAAAGTGTGTTTGTGACGTACTCACTCATGAGTATGAGCCATGGCTGTGCTATTCTCT
CAACATTTGTAGCGCCGCGCGAGTGCCTCATCTGACTGTCAAGGATGAGGGCTCTTCCACC
TCAAGGACACAGCCAAAGGCTCTGTGAGGAGCCTGGGAGCCAGGCTGGCCCTGCCCTGGGC
TGGAGGGACACATGGGGCTCTGTGGGAGCAAAAGGAGGTCTGTCTTCTGGGGAGAACCACTT
TAAGTCACTGCCCTCTCTTCTGGGGGAGCCAGTCTCTGTAAGACAGATGTGCGCATTTGA
GCTCAGCAGAAGAGGCAGAGTGCCTACTGGGCAGACACAGAGCTGAACCGTGC CGCGCGGCGC
TCTTCAGCAAAAGTTGAGGGCTATGGAAGTGTATGCACTGCAAGGACCCACACCATTCGA
GTTACGCCCTGACCCATCCGAGACACAAGGTCCTCAATGTGCTGTGGCTGTCACTTGCAG
GGAACCGACCAATTAAGTCTGTACAGATGCTGCGCTCTCTGCTTTCAAGCCAGGGGTGTCT
CCTCAGATGATTAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCAT
GTTTGGTCTGAGGGGCTATCAGCATACTCCCATCAGCATCAAGAATGCCCGGCTGTCTCAGC
ACTACAAGGCCAGCCTACTGCGACTTTCAACCTGTTTCCGGAGGCCAAGTTGTGCTGTGTT
CTGGAAGAGGACCTGGACATGCTGTGGAATTTTTCAGTTTCTGAGCCAAATCCATCCACCT
CTTGAGGAGGATGACAGCCTGTACTGCATCTCTGCCGTGGAATGACCAGGGGTATGAACACA
CGGCTGAGGACCCAGCAGCTACTGTACCGTGTGGAGACATCGCTGGGCTGGGCTGGGTGCTC
AGGAGGTCCTGTGACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAGCTCTGGGA
TTGGACATGTGATGCGGATGCTGACAACAAGCCGGGGCCAGATGTCATCTCCCTGACG
TTTCCGATCTTACCACTTTGGCATCGTGGCCTCAACATGAATGGCTACTTTACAGAGGCC
TACTTCAAGAAGCACAAGTTTCAACACGGTTTCCAGGTGTCAGCTCAGGAATGTGACAGTCT
GAGGAAGAAGCTTATGAAGTGAAGTTTCAAGCGCTGTCTAGTAGGCTGAGGTTCTGTGACC
ACAGAAGAAGACCTTTGTGAAGTCTTTCTGCGCAGGACAGAGGCCACACTAGTGTGGCC
TTTATTGCAATGGAGAAAGATGATGACTTCAACCACTGGACCCAGCTTGCCAAGTGCTTCCA
TATCTGGGACCTGGATGTGCTGTGCAACCACTCGGGGCTCTGTGGAGATTGTTTCCGAAGAAGA
ACCACTTCTGGTGTGGGGGTCCGGCTTCCCTACTCATGTGAGAAGACCCACCTCAGTC
ACCCCAATTTCTGAGGCCACCCCAAGGAGAGGGAGGCCCCAGGAGCCCCAGAACAGAC
ATGCAGCCTCTCCAGGACCTGCGGGGCTGGGATGTGTACCCCGAGCTGGCTAGGCCCT
TCCCTCCATCTGTAGATTTTGTAGATGCTGTTAGGGGCTGGGGTACTGTTTAACTA
TGAGACTTAATTACTAATCAAGGGGAGGGTTCCCTGCTGCTCAACACCCCTTCTGAGTT
AAAAGTCTATTTATTACTTCTTTGTGGAGAAGGCGAGAGTACCTGGGAATCATTACG
ATCCCTAGCAGCTCATCTGCCCTTTGAATACCCCTAGTTTCCAGGCCTGGCTCAGAACTTA
ACCTTTTATTGACTGCTCTGAGGCGCTTGAAGAACAGGCCAAGCTGGAGGGCTGGATTTCT
TTTTTGGCTGGAATGCTGCCCTGAGGCTGGGGCTGCTCTTACTCAGGAACACTGCTGTGCC
CAACCCATGGACAGGCGCAGCTGGGGCCCACTGTGACACAGACTCACTCAGAGACCCCTTA
GACACTGGACAGGCGCTCTCTCAGCCCTTCTCTTTGTGCAGATTTCCAAGCTGGATAAGTT
GGTCATTGATTAATAAAGGAGAAGCCCTCTGGGAAAAAATAAATAAATAAATAAATAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGA VFLLVTVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLF LNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGD PVLLKTDVPLSS
AEEAECHWADTELNRRRRRC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEEPM DVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFP EAKFAVVLEEDLDIAVDFFSFLSQSIH LLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMW MRMQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKKHKTNPVPGVQLRNVD SLKKEAYEVEVHRL LSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

GGAGCGCGTGGGCTGCGTGGTGGGAAGGCCTAAAGACTGGAAGCCCACTCTCTTGAACACCACCACT
 CTTGTTAAAGCAACTAAGCACCACTTTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGTTGAGGAGCAATGAGTGATGTTATCTCATTAGCTGCTGCTGTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCTTGCTGTGTAATTTCTCAGGAGAACAGCTGAAGCTGGTGACATGTTTGTGA
 GTGCTGGCCCTTCTCTGTGGAACTGCTCTGGCAGTCATGCTGCTCAGGAAGTACATGCCCTTTATGAA
 GATATTCTTGAGGGAACAACACCACCAAGCAAGTGAACACATATATGTGATTGCATGACACAAGACGAG
 AGAAAACTCAGTTGTCCATGAACATGACACAGCCACGACATGACATGCCTATATTTGGT
 TTTCCCTCGTTTGGGCTTGCTTTTCATGTTGCTGGTGGACCAGATTGGTAATCCCATCCCATGTGCATCT
 ACTGACAGCTCAGAAGCAGCAAGGCTAGCAATTCACAAATACACCACAGCTGGGTCTGGTTGTCCCA
 TGCTGCAGCTGATGGTGTGCTTTGGAGCAGCAGCATCTACTTCACAGCAGGATGTGCAGTTAATGT
 TGGTTTGGGCAATCATGTCTACATAAAGGACCAAGCTGCTTTGGCAGTGGTTTCTCTTGATGATGCTGT
 GGCTTAGAGCGGAATCGAATCAGAAAGCATCTGCTGGTCTTGCATTTGGCAGCAGCAAGTATGTGTCAT
 GGTGACATCTTAGGACTGAGTAAAGACATGAAGAAAGCCCTTTCAGAGGTGAACGACGACGGAGGTGG
 CGTGCCTTTTCTCGCCGGGACATTTCTTATGTTGGCAGCATGATCTGCCCTCTGAGGTGGGGCGA
 ATAGGCAAGCAGCAAGCCGATGCCAGGGAGGAGGCGCTCAGCCGCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTTGCCATCCCTCTCATCTCTGTCAGTAGGACACAGCATTAAGATCTCAAGGTCCAGC
 CTGGTCCAGGGCCGTTGGCATCTCAGTAGAGAACGCGGACGCTGACAGCTACTACTCTTCCTGACCT
 TCTTGCTCTCACCCTGGCCATCTCTACATGATTTCTTAGCTAGAGTCAGAGGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAGCTTTTAGAGTAGAAGAACATTTACGTTGCGATTAGCTATAGACATCCCATTTGTGT
 TATCTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCCATTATCTCAGGGAAGATG
 GAATTTAGTTTAAAGAAAGAGGAGCAACTTCATACTAGCAATGAATATGATTAATGAATAACAGT
 GTCTGTGAATTAAGCTATGCTCTCTTCTCTAGTTTAGAGGCTCTGCTACTTTATCCATGTGTTTT
 AACATGGTTCCCAACCTGTAAAGCTGGTGGCTTTAGCATCTATGCGCACATCGGTTGATGAAGGTCATA
 GCACCAACTCATAGATGCTAAAGTGATCTAGTTAATCTGGGATAGGTTGAGAAAGTATAGC
 AAGACACTGTAAAGCTCTCTTATGCTCAAAAGGAGATTCATTGAAAGGAGTGCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCTCTCTGAAATCAGAGCTGCCATTGCAATGAATGGAGCAGGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAGTCTCTCTTTGCAGAAAT
 ACCTGTCTCCACATCTCAGAGAGGAGGCAAGTTCTAGTATTTTCAAGTCTAGGCTTCTCTCTCAAGAA
 CAGTCAGATCAAAAGTGTCTTGGAAATTAAGGATATAAATTTAAGTGAATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTAAAGACATACCAAAATGATAGTTGTGCTTTTTTTTTTTGTTTT
 TTTTTTTTTAATATTTTCTCTAGCAGTACAGCAATCCTCTAGGACCAATAACTAGTGCAGCTTT
 GCGCAGAGCTGTGCTCTCATACATCAACCTCTGTAGCAAGATGATCATAAATGAGAAGTGTGTGCTCA
 TTGATTTAAAGCTTATGGAATCATGCTCTGTGCTCTGCTGCTTTTCTGCTTTTCTCTCAACTTT
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATTTTGTGTGGGATGAAT
 CTTATCAGGACACCACTCTCGAAGCTGATAATGAAGATAAATATATTTATTTCTTATCCCTCT
 CAAGAATAATTACCTTTGTGTCAAAATGCCGCTTTGTGTAGCCCTTAAATACCACTCCTCATGTGTAA
 ATTGACACAATCACTAATCTGGAATTTTAAACAAATGAGATAGCAAAAGTGTGTAAACAGTAGGATA
 ATTTTTTTTTTCAATTTGCAAAATTTTGTAAACCTGCTGTGCAAAATAGTGTATATATTTGAT
 TATTTATTTATTTTACTTCTTATCAACCTTCAAAACAAATTACATAGGCGGAACCAAGCATGTT
 TCTCAGGCGCAGTGGACGTAGTAGTTTGTAAACACGTTTTCTAGCAGCATAGCTAGCATGCCATGCT
 ATTTATTTCTCTCATGAATTTGTCTAGTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT
 GCGCCAGTGGAGGAAGTAGCACAATAGGATACAGTTGATGTAGCTATGGCAACAATTGGACATACA
 ATTTTACTACCAAGAAAGGTATAGTATGGAAGTCCAAATGAGCTCTTCTGATGGATGTAAAGCT
 GACTGGTGTGAGACTTGAAGTTTCACTAGTCCCTCAAACATATATGGTTGCTAGATTTCTCTCTGGA
 AACTGACTTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAATA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFMLHAGLEARNRIRKHLVFFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCGATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGCTCCGAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCGATTAAAGACCTGCGAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACAGAGGTGCCACAAGGAAGGAAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCGAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCTATCCCCACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAAGTGAATCAGATATTTACAAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQLQALSEPQPRLQAAGLPHTVEVPQGKGNVLGNSKSQT PAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRVPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGAGAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTGCTCACCCTTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGGCATGGGGAGGCCAAGGGAAACCTGGGCTGCTGGATGGCTCCGATTTTCCGGGTTGTGTTGGTGTCTGA
 TAGATGCTCTGCGATTGACTTCGCGCAGCCCCAGCATTACACGCTGCCATGAGAGGCTCCTGTCTCCTACCTCT
 TCTGGGCAAACTAAGCTCTTGACAGGATCTGGAGATTACGCCCCACCATGCCGGCTCTACCGATCTCAGG
 TTGACCTCTCTACACCCACCATGAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCCTACCTTTATTTGATGCTG
 GTAGTAACCTTCGCGAGCCAGCCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAAGTGCAGGAAGGCGTAG
 TCTTATGAGAGATGATACCTGGAAGACCTTTTCCCTGGTCTTTCTCCAAAGCTTTCTTCTCCCATCCTTCA
 ATGTACAGACCTAGACACAGTGGCAATGGCATCTGGAACACCTTACCCACCATGGACAGCTGGTGAATGGA
 ACGTGTGATTGCTCACTTCTTGGGTGTGGACCATGTGGCCACAAGCATGGCCCTCACCACTGAAATGGCCA
 AGAACTTAGCCAGATGGACAGGTGATCCAGGACTTGTGGAGCTTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCGACACCCACAGAGGACCCAGAGTGATTCTCAAGTTAGCCTTGTGC
 CCACGCTGGCCCTGCTGCTGGCCTGCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGTGAGGACTCCACGCCCACTCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCCGATTTCTCATACCTACTCAGTGCTACTCAGGACCTTCAAGTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGCTTGAGGCCACACTGCCGACTGTGA
 TTGCTGAGCTGCAGCAGTCTCTGGCGGGAGCTCGGGCCATGTGCATCAGCTCTTGGGGCTCGTCTTCTCTGGTCC
 GCATGCGGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTCAGTGGGCAATATCCC
 CAGGCTTTCCATTTCTGCCCTTACTCTCTGACACCTGTGGCTGGGGCTGGTTGGGGCCATAGCATGCTCTGAGC
 TCTTGGGAACATTAGGACTGAGCTAGATCTAGTGTCTTAGGGCTGTGGCTGAGCTGAGCTATTCTCCCTTT
 TTCTTGGGAAGCTCGGGCTGGCTGGGGTCCAAAGAGGCCCTTGGCAACCTCTGTTCCACTCCCTGGGCCCTGCC
 TTGATCTCTGCTCTTTTCCCTTGGCTGTCTTCTCTCTGATATTTTGTGCTGAGGCCAGGCCACCCCTCT
 TCTTTTGGGCTCATTTCACTCTGCTCTCTGTTCTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACTTAAGCTAC
 TCACAATGCCCGCTTGGCATTTCAGCCACAACAAACCCCAAGGCCACATATGCCCTGAGGCTTG
 GAATTTGGTGTCTTTATGTACAAGGCTAGCTGGGCTTTTCATGTTGCTTCCCTGAAGAGACCATGTTGGCACT
 CCTCTGCTGGCTGAGTCTCTGGCATCATGGTGGTGGTCTGAGCCAGAATTTATGATATGAGCTTGTGTGG
 CGGCGCTGGGGCCCTGTAGCTGCCGTGGCTTTGGCTTCGCGCTATGGTAATCTCAAGAGCCCGAGGCCAC
 CCAATGCTCTTTGTGGCTGGGACTGCCCTAATGGCATTTGGTACTGCTGCCCTACTGGGCATTGGCGTGGGGG
 CAGATGAGCTCCCCCGCTTCCGGGTCTGGGTCTTGGGGCATCCATGGTGCTGCTCCCTGGGCTGTAGCAGGGC
 TGGCTGCTTCAGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGCTGGTGAAGGCTGGGGCAGGCGCTCCAA
 GGACAGGACTGCTCCTACTCCCTTCTCAGGCCCCCCTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
 TCTACCGACACATGAGGAGGAGTTCCGGGGCCGGTTAGAGAGACCAATCTCAGGCTCCCTGACTGTGGCTG
 CTATCAGTTGGGGAGTTCTACTCAGCTGCTATGTTGTCACAGCCCTCACCTGTTGGCTTCCCATCTCTGCTGT
 TGCATCGGAGCGCATCAGCCTTGTGTTCTGCTCTGTTTCTGAGAGCTTCTTCTCCTACATCTGCTTGTCTG
 CTGGGATACCCCTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCACTCGGCTTGGGCCCTCATGGCCA
 CACAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGCCATCCATTGGCATGCAAGCTTCTGGGATATCC
 CAGAGGCTCAGGCTCTGACTCTTGGCTGCTGCTTGTGCTAGTGGGAGCCAACCTTTGCTCCCACTCCTCT
 TTGACGTAGTTTGGCCACTGCTCTGCTCTGGCTTTTCTGTGTGAGAGTCAAGGGCTGCGGGAAGAGACAGCAGC
 CCCCAGGAATGAAGCTGATGTCAGAGTCAAGCCGAGGAGGAAGAGGAGCCATGAGAGATCGGGCTCCGGG
 ATGCGCTCAGCATTCTATGAGCAGCTGCTGACAGCTGGGCTCAAGTACCTTTATTCCTTGGTATTAGATTCT
 TGGCTGTGCTTGGCAGCTCAGCAGCTCTTCTGCGCATCTCATGGTCTGGAAGGTGTTGCCCTAAGTTCAAT
 TTGAGCTTGGGCTTCAATTGTGAGCAGCGTGGGACTTCTCCTGGCCAGCTAGCTTTGGTGATGAGAGTGGATGGT
 CTGTGAGCTCTGGCTTCCAGCAGCTATTCTTGGCCAGCAGAGGTAGCCTAGCTGCTGTGATGAGAGTGGCT
 ACAGAGAGTGTGTGAGAACAGTTAGCCTGGCCTGTACAGGTACTGGATGATCTCAAGACAGGCTCAGCCATAC
 TCTTACTATCATGAGCCAGGGGCCGCTGACATCTAGGACTTCAITATTTCTATAATTCAGGACCAAGTGGAGTA
 TGATCCTTAACCTCTGATTGGATGATCTGAGGAGACAAGGGGGCGGTCTCCGAAGTGAATAAATAGGTCGGG
 GCGTGGTACTTGCACCTATAATCCAGCACTTTGGGAGCAGAGGTGGAGAGTCTTGGTCCAGAGGTTCA
 AGACCAGCTGTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLFPWGSQGKPGACW
MASRFSRVVLVLIDALRFDAQFQHSHPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLKIQLTSAAGRRVVFMDGDDTKWDLF
PGAFSKAFFFPFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKGPHHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAAFLYSPAVFPST
PPEEPEVIPPVSLVPTLALLLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAQASALHNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFASKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFFPIPGPVLLLLLFLRIA
VFFSDSFVVAEARATPFLGSGFILLVVLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCRTLGLFHRCPPEETPVCHSSPWLSPPLASVMGGRKKNLYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPLRLVLVSGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLLHAERISLVFLLFLQSFL
LLHLLAAGIPVTPPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAVFVGPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWVKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT
 GTCTCTGGTGGTTTGCTTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTGT
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACACACGCTGGTGTCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCCTTCGTCGCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGTTATGTTTTG
 CCCATATCTATTACCGTGTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAA
 GATTCCTTTGTGCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTGTATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAAACAGTCATTGAATATGA
 ATATGATGTGAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCC
 CAAACGTTACAGTACTCATACCCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC
 AAACGTCAGGCTGTGTATTCTTCGCTGTTCAGCTTCGACCAGGATTAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGT
 TATATGTGCAGATGGAACATGATGCCAACACTTCTTTTGCCTTTTGTTCCTGTGCAAC
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGT
 GTTCTATGCAGAGGAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTGAG
 TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPSPRRAPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFD
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFQDSEGCEPSEGDGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
 TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
 GATGCTGCCCCGTAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
 TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
 GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCTGAGTACTGCGGAGCCACCCAGCAGG
 TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
 TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGTCTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
 TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCTCGTTCCTTCTCGGGCCTCTGGTGCGCGACCCCAAGACCCCGAC
 GTGTACACGAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
 CCAGCCCGGCCCTGCTGGGACCACCAGGCCCCAGGAGAAGCCGCCTGAGCCACAACCT
 TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
 AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGACGGTGGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGRF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCLTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGGCTGGGCACGGTAG
 CAGGCGCCCGCTGCTGCTCAAGGACTATGTCACCGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAC TGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCGAGCTGGCGGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCACGTGAGGAGGCCAGCGGTGCCTGTCCGGGAGGGTTCCAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC
 TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLLTNLLLDKLGASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPFIWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACAGCTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCAAACGCGCTGCA
 GTCTGAGCTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCTTGATGCGGCTGCAGCAGTGTACATGCTCAATGTGAAAGGCCTGGCCCCAGGCTGCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTCCGGGACAGGA
 ATGTTTCTGTGCGCCTCAGCCTCTCTCGGGAGTTTCTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACCTACGAGGGGC
 TATGTCAGACCCCTGGGTTCCAGCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCTCTAT
 GAGACCAATTCCAACGCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGCTGGTGGCATCAGGGGAGAACGAGTTACAAAGTGGAG
 TACCCGATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA
 CCACCGCATTGCTGCCCTCACAGGCTTGATGTCCGGGCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATTGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTCTGCTGGTGGGAGATAAGTGGGTGGCCAAACAGTGGATACATGAGTATGG
 ACAGGAATCCCGCAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGAAATCAGAGGC
 AAGGGAGAGGTTGTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCCTGAGAGGGAAGTTCTGG
 AGTTCAGATACCTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCACAGGACCAAGAAGTGGAATGAGGACACCTCAGGAG
 GGGCTAGCCTGACTCCGAACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGAGAGTGTCCCCCTCCCAAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTAAACAGTCATTAAAA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAFERRLLGLLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTSAITDLYSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEFWLQ
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFTYANLSVPVVRNAALFWW
 NLHRSGEGDSDLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGCTCTGGGTTTAAAGTTCTCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGAGCCGAGCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
CGCCCAGGATCCCGCGCGGGGACTCGGAGAGGTGCGCTACTGCGCGCGCTTCTCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCTTGGTCTCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCCTTCC
TGGCTCCAGCCATCATCTCATCTCTCTGGCGTCGTATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCTGAAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCTGGAACCTTGCGCTGTGGGTGCCCCATCA
CCTGCTGCATCAGGAACACGACAGAGTTGTCAACACCATCTGTGGCTGACAAACTATCGAC
AAGGAGCGTTTTAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCGTGATCAT
CTGGTTCTATGGACAACATACACCATCATGCGGTGCATCCTCCTGGGCATCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACC CGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAATTAGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCTGTGTGTAGTCCCACGGCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGGCTCCCTAAGAGGCTTTCCTCCAGGCCTGGGCTACAGGGGAGGGA
GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC
CTCTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTCTGTAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTTTCCGCGATGTCCTATTCTTGCTCCCTTCCCCAACAGGTTTGTAA
TCAAACAATAAAACATGTTTTGTTTTGTTTTTAAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AAILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVI IWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGP GAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGCGCGGCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTGCTCTCATCTCGGCCAAAAGTCATCAAAGA
 AAAGTGCACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGAAAAGCCAGCCGGAGGCATCCCTGTGTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGGTGAAGGTCAACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGCGCCACCCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTTCCAGCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCTGTGG
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCTAATCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCTGTCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLIILGPKVIKEKLTQELKDNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLNALAKQVMN
LLVPSLPLNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAlKGDTIQLYL
GAKLLDSQ GKVTKWFNNSAASLTMTPTLDNIPFSLIVSQDVVKAAVA AVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGQQLIILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEI IHSIL
LPNQNGKLRSQVPSVLVKALGFEEAESSLT KDALVLT PASLWKPSSPV SQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGGTTGGCGGTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTGCAGCGTTCCTCAGCCTCTGCCCAAAGAAAGAGAGATGGTGTTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAGACCTGTAATAAGAAATGAATGGAGACA
 AGTTCGCTCGCCTTGTGAAAGCCCCACCGAGAATTACTCGCTTATCGTCATGTTCACTGCT
 CTCCAACATGCATAGACAGTGTGTCGTTTGAAGCAAGCTGATGAAGAATTCAGATCCTGGC
 AAACCTCTGGCGATACCTCCAGTGCATTCCCAACAGGATAATTTTGGCATGGTGGATTTTG
 ATGAAGGCCTCTGATGATATTCAGATGCTAAACATGAATTACGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGAAACCCAAACGCGGTGATACATATGAGTTACAGGTGCGGGTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAATGATGCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTTGGTGGACTTGTGTAT
 CTTTCGAAGAAGTAATATGGAATTTCTCTTAAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTA
 GCTGAAACACACATTTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAATCGTGTGTGTTTGAAGAAGAAATGCAACTTGTATATTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAATAAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATATATAAAATTTGAAAA
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAAACTACTTTAGTTAACTTTGGTCACTCTGAT
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCATCTTAGCTTCTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTCTCTTTGAGTAGAGAAATATGTGTGTCATGTGGTCTCTGAAAAATG
 GAACACCATTCTTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAAGTACCTTGATTAGAAA
 GATTTAGATTTCATTCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAAAACTAGTGTAACCTTATACATGGCCTAAAAATGTTTCTCAAAATTAGAGT
 TTGTCACCTTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTCAGGAGTTCGAGACCATCTTGCCCAACATGGTGAACCCCGTCTCTACTAAAAATAT
 AAAAAATAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCAGCCACTGCATCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRNPVIRMNGDKFR
 RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
 SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
 AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
 PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
 VLFFSWMLSI FRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250

FIGURE 75

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGAGGCTCTCAGAACCGCTACCGGCGCATGCTA
 CTGCTGTGGGTGTGGTGGTTCGACGCTTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTCTGTGAGCGACTCCTTCGATG
 GAAGGTTAATCTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG
 ACACGTGGGACTTCCTTTCTGAATGCCATCACAAACTCTCCAATTTGTTGCCCATCAGCGCG
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAAGGCTCTAG
 ATCCAAATTTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAAACAGGA
 CTAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTGTATTATTTACTTGGGATTAAATTTACCACACCC
 TTACCTCTCACCATTCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
 GGCTTGAAGAAAGTGTCTCATGATGCCATCAAAATGCCAAAGTGGTCACCTTTTGTGAGAAATG
 CACCTGTAGATATTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGA
 AATTAAGAAATATTAGACATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACCTCTCA
 GACCATGGAGAGCTGGCCATGGAAATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGTGATGGGACCAGGAATTAAGCCCGGCTACAAAGTATCAAAATG
 TGGTTTCTCTTGGGATATTTACCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATCTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAAATGAACATAAAGT
 CAAAAACCTGCATCCACCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCACTGGAAATATATAGCCTATTCGGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTCTCGATCCAGATGAATTAACAAATGTTGCTGTAAATTTCC
 AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCCTAAAGTTTCTG
 CTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT
 TATTCAAACGTTATAGCAAACTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAATGCAATTTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTAATTT
 AAATGAAACAGTTTTAATAATTACCAAGTTTTGGCCGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCTTCTGGC
 CAACATGGTGAACCTGTCTCTACTAAAAATACAAAAATAGCTGGGCGCGTGGTGACACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGACGTGAGCTGAGATTGCGCCACTGTACTCCAGCTGGCAACAGAGTGAGACTGTGTCCG
 AAAAAAATAAAAAATAAATAAATAAATTAACCAATTTTCAATTTTGTAAAGATGTAGTG
 TATTTAAGATAAAATGCCAATGATTATAAAATCACATATTTCAAAAAATGGTTATTATTTA
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAGGATTGAAGCAAATCTGTGA
 ACAGTTATGTTCTTCTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAAT
 AGTTGTATGTGAGCATTTGATGGTGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINE
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGVRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLGNLPHYPSPSSGENFGSSTFHTSLYWLEKVSFDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVII
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPIKAGLQVSNVSLVDIYPTMLDIAGIPI
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNNHWKYIAYS DGAS
ILPQLFDLSSDPDELTVAVKFEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCATGCTGCTCCCCAGCTGGAAAACAAGTTCATTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG
 TGTGACATCTATAGCACCTTCTGGGCCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCTTCTGTTGCCCTGGAATCTTCATGGGATCCTACGGGA
 CTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCATTCCTACAGCCTGACAGGGT
 ATG**TGTA**GAAGAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATCCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAAC**TGAAATAAA**ACCATCCTACGGTATCTCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGVIILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSSPRPGQPPKVKSEFNYSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAC TGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCT**TGA**GAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEFWLCQPAFRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISKCESRRRFF

Signal peptide:

amino acids 1-25

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGTGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCACCTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTTACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

bioRxiv preprint doi: <https://doi.org/10.1101/2021.01.27.428888>; this version posted January 27, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGGCACCAGAAGTTCTCT
 GCGCGTCCGACGGCGC**CATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGCAGAACGTCACCTTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCGAGGTGCAGACCTGCTCAGAGCGCCGCCCATCCGCAACCTCAGTTCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGTCTG
 GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTTGCCCTCCCCCTCATCTGTCTCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCCCGGTGCCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACC
 CCGGCTTTGAAGCCTCACCACTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
 CTCCAACCTTTGAGGTCATC**TAG**CCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGGTCTGAG
 ATTCFCCCTAGAGACCTGAAATTACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCGTTTGGCCCGAGGCTGCTCTTCTGTG
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCATGGCCATCGCC
 ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC
 ATATTGGGCGCATGGTGCCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCCGCCCTCCCCATCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLLGPVVK
GHDVTFYKTYRSSRGVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLASAD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVVPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLEPSTPLSPPGPGDVFFPSLDVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTCCACCTTAGACCTCCCTTCTGCCCTCC
 TTTCTGCCCACCGCTGCTTCTGCCCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCCGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCCGA
 CTCGCTCCCGGACCAGCGGCCGTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC
 TCCTCCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGCGCAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCGTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCTCCACTGTCCGCGCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTTCC
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCCTCAC
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGCGCTCAGCGCCCCCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTAATCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCTTGGCGTCAACCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGGACAAA
 GCAGACCTTGGCCACAGTGAGATCAGTTCTACAGGTGTCCCAAGGCACCGGGCCGGGTCTT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAG
 GAAGTCACTGGAACGTCTTCTAGCCAGACCTTGGAGTGAAGGTACAGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTTGCATTACCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYPGESWH PYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGC GGCTGCGGGGAGCTCCC
GTGGGCGCTCCGCTGGCTGTGTCAGCGCGGCCATGGATTCCCTTGCGGAAATGCTGATCTCAGT
CGCAATGCTGGGCGCAGGGGGTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
AGCGGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGCGCAAGGCGCGCCAGCGGGAGGTACCGGT
GAGACCGGACTTGCTCCGTGGGCGCCGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTTCGTGGGCCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTTCCCCAAACCTTGGACTGACTGCTTTAAGGT
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAACGAAAGAACCAATAAAA
TCATGTTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

bioRxiv preprint doi: <https://doi.org/10.1101/2021.01.14.428888>; this version posted January 14, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 89[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSWGPLQGQHHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQ
QWDTPCPRENAEAAFVICGLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTCTCTAATCCAT
 CCGTCACCTCTCTGTCACTCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACATTAC
 TGTGTTGGATGCTGGCCTCTATTGGGTGCAGGATTAGTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTT
 GATAGAGACATCCAGTACTCTGTGAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTGTTGATGTGGAGATCTCTGTGACCGTCCAAGAGAACCGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCCAGTGGAATAACAGGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACAAATAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAAGTCCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAAGCAACAGTGAGTCTCTCTCACAGGCAACACGCGCTTCTCTCCGAGG
 GTGAAATGTAGGATGAATCAGATCCACATTTCTTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCGGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCAATATATTACACTTTCAGTA
 AAAAA

FIGURE 92

MALMLSIVLSLLKLGSQWQVFGPKPVQALVGEDAAFSCLSPKTNAEAMEVRFRRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLNITVLDAGLYGCRISQSYYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFSQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRINGEHLTYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQSESEKEASWQRASAIPESTSNESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA
 ACGAGGAGAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGGCTGCCGAGCCTGGCGGCCCTCGCCCTGTTGTGTGCTGCGCCGCCGCCGCCGCGCG
 CCGTCGCTCAGCCGCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG
 GACGCGTCGCGGGGCCCCGGGTTGCGGGGCGAGCCGACGCCACCCCTTCCTTAGGGCGACGGC
 TCCCAGGGCCGAGGCCCGGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC
 ACCACCTTTCAGGCGCGCTCGGCCCTCGCGGACCACCCCTCCGGCGGCGGAACGCATTC
 GACCACCTCTCAGGCGCGGACGAGACCGCGCGGACACCCCTTCGACGACCACTGGCCCGG
 CGCCGACACCCCTGTAGCGACACCGTACCGGCGGCCACGACTCCCCGAGCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCAACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACCTGTGAAACC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACCTGAAGTTTATT
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACTTTTATCTCTTACTTTTATATGT
 TATATTTAATGTCAAGGATTTAAACATCTAATTTACTGATTTAGTCTCTCAAAGCAGTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAATTTTATGGGAAAAAATTTATGAAGAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAATTTCTACATTTGTTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCATATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAAG
 TAGATTAAGCAGGAATATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTTGCGTTGTACTGCACGTAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACTTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCCCTTTCACCTGAGCTGTGTTCTCTCAAG
 GTTGTGTGAAGATTAATGAGTGTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTAACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTATGGAATATTGTATCATATTTGAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGCTCTCTACTAAA
 AATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGAGGCT
 GAGGAGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGLALLCCAAAAAASASAAGNVTTGGGGAAGQVDASPGPGLRGEPSPHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPPLWATAGPSSSTTFQAPLGPSPPTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTVPVATVPAPTTPTPTDLPSSSSSVLPTPPATEAPS
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**GATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCCTGGCCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGTGAGACTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQA~~V~~WLGR~~L~~DPEQL~~L~~GPWYVLAVASREKGFAMEKDMKNVVG~~V~~VVT
LTPENNLRTLSSQHGLGGCDQS~~V~~MDLIK~~R~~NSGWFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTTACCCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCTGTGAGCAG
 GGGACACCCCTATGATCTCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGCTTTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCTGTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTACGCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCCAGCT
 TCTGCCCCTCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATGA**G**AAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTQVTFPGASVTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNGSSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSSAQGPLTEPWAEDSPDQPPPASARSSVGEGLQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSFVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYQLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTCGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAAGACGCGGCTACTCTGTGG
 GCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCATGCTGGCACCAGCTGCCTCATTTCGGGCTGGGGCAGCACGTCC
 AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATACCATCATTGAGCACCA
 GAAGTGTGAGAAGCCTACCCCGGCAACATCACAGACCCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
 AAGAAACCCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIHQKCEENAYPGNITDTM
VCASVQEGGKDCSCQDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTAGATTTCATTGTTT
 TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
 GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAAATGGTTTGTTCTTGTTGGGCAAGTCATAAAAGGCCATA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
 AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAGA
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
 GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAAGTCACTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
 TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHGPKWFVLGVGVQVIKGLDIAMTDMCPGKRRVVI PPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDFKKNDDHGDGFISPKYENVYQHDEL

```

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACAAAACCTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPILLPLGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

106/249

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGGCAGAGGTGGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC
 ATCACCACCCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGTCTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTGCAAGTATGTGGAAGTGGATCCGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCCTCCACCTCCACCCCAACCCCTTAACCTGGGTACCCCTCGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTCTTGGAACCT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSSGGPLVCGGVLQGLVSWGSVGPCQDGI PGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17



FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
 GCTCAGACCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCAGACTTTGTGAA
 CATGATGCTGGGGAACGGTTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCTCTCTCTCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGCGAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTTCAAGAACTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTTGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTGCTCTCTGCGCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCGTG
 GGGTTTGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMKELGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLV
MFEGKANESSPKFVGPPPERDIASLP

110/249

FIGURE 111A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCACACATGCCCCCGGGTGGGCAGGGGTGCGCGCCGCGTGCAGCGCC
 CGCTGCGCGCTGGCCTTGCGCGCTGGCGAGCGTCTGAGTGGGCCTCCAGCCGTCGCGCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTC
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATATATCACCAGGATG
 ACCAAGATTGGAATCTTCCTGGGCTCAAGAACCTCCGAGTCTTGCACTTGGAAAGACAACCGAT
 CAGCGTCATCGAGAGAGGCGCCTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTTGAGTGAAGAACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT
 GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
 TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACGAGC
 TTCAACCACATGCCGAAGATCCGAACCTGTCGCGCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTACACTCT
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAGAAGGAGTACGTG
 TGCGCCAGCCCCCATCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCTGCGCTTCCGCC
 CTGCCAGTGCAGCAATAACCTCTGGAATGTCGAGGAAAGGGCTTGATGGAGATTCTTGCCA
 ACTTGGCGGAGGGCATCGCTCGAAATACGCTAGAACAGAACTCCATCAAAGGCATCCCTGCA
 GGAGCCTTCCACCGATACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCCGA
 TATTGCTCCAGATTGCTTCCAGGGCCTGAAATCACTACATCAGTCTGTGCTGAGGAACA
 AGATCACCAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
 AATGCCACAAGATCAACTGCGCTGCGGGTGAAACAGTTTCAGGACCTGCAGAACCTCAACT
 GCTCTCCCTGTATGACACAAGCTGCAGACCATCAGCAAGGGGCTCTTGCGCCCTCTGCAAT
 CCATCCAGACACTCCACTTAGCCCCAAAACCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
 CCGGACTACCTCCAGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCGCCGCGCGG
 ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGCAGAAGTGTGCG
 TGTGAGGCGACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
 TGAATATGTCACCGACTGCGACTGAATGACAATGAGGTATCTGTCTGGAGGCCACTTGCA
 TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCATGGAGCAGCGACGCTGCAGGAGCTGATGCTGCAGGGAACCACT
 GGAGACCGTGCCAGGGCGCGTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
 TAACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCAACCAGCTTGTCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGCGCGATCGTCACTGGGAACCTCAGTGGCCAGAGCCATTTTCCCTC
 AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGAT
 GCAGCAACAAGGGGCTCCGCGCCCTCCCGAGGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACTAAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTGACACCTTCAACATGATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCTTCAAC
 GGGCTGCGGTCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGTTCCTGAAGG
 CTCCTTCAAGCACTCAGCTCTTCCATCTGGCCTGGGAGCCCAACCACTCCACTGTG
 ACTGCAGTCTTCCGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCTGGGATCGCC
 CGTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCAACCCCAACCCAGCTCCT
 CCAGTGCAAGGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCTGCCCTTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTTCCCC

TACAGCTACAAGGGCAGGACTGCACTGTGCCATACACACTGCATCCGAAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCTGCCCTT
 TGGGCTTTGAGGGGACGGGTGTGAGATCAACCAGATGACTGTGAGGACAACTGCTCGGAA
 AACATCGCCACTGCGTGGAGCGGATACAACAACTACGTGTATCTGTCCGCTTAACACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCATTGTGTGCTGAGCTGAACCTTGTGACGAT
 AGGCGCAAGTGTCATCCCCCTGGACAAGGATTTCAGCTGCGAGTGTGTCCTTGGCTACAGCGG
 AAGCTCTGTGAGACAGCAATGATGACTGTGTGCCCCAAAGTGGCCGACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCGCCCGGCTTCAGTGAACTTCTGTG
 AACACCCCCACCCATGGTCTTACTGCAGACCAGCCCATGCGACCAGTACGAGTGGCAGAAC
 GGGGCGCCAGTGCATCGTGGTGCAGAGGAGCCCACTGCCGCTGCCCAACAGGCTTCCGGCG
 CCGGACATGTCGAGAAGCTTACATCTGTCAACTTCGTGGGCAAGAAGCTCTCACTGGAACTGG
 CCTCCGCGCAAGTGTCCGACCCAGGCGCAACATCTCCCTCGAGTGGCCACTGACAAGGACAC
 GGCATCCTTCTCTACAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAAGGCCAGCT
 CGCGCTGTGCTATGACAGGCTGAGTTCCCTTCCAAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAAGTTTCACAGTGTGGAGCTGTGGAGCTTAACACAGCCCTGAACCTAGTAGTG
 GACAAGGAACCTCAAAGAGCCTGGGAAAGCTCCAGAAGCAGCCAGAGCTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCCCTTGCGCCAGGGCACGG
 ACGGGCTCTAGGCGGCTTCCACGGATGACATCCATGAGGTGGCGCATCAACAACGACTGCGAG
 GACTTCAAGGCTCTCCCAACAGTCCCTGGGGGTGTCAAGAGCTGCAAGTCTTGACGCTCGGT
 GTGCAAGACGCGCTGTGCCGCTCGTGGAGAAGGACAGCGTGGTGTCGAGTGGCCGCGCAG
 GCTGGAGCCGGCCCACTTCGCACAGGAGGCGCCGCGGACCGCTGCTTCGCCACAGATGCCAC
 CATGGAAATGTGTGGCAACTGGGACCTCATACATGTGCACCTGTGCCAGGGCTATGGAGG
 GGACTTGTGTGACAAAGAATAGCTTGCCAACTGCCTGCTCAGCTTCAAGTGTCAACATG
 GCGAGTGGCAACTCTCAGACAAGGAGGCGGCTTACTGCTGTGCGAGCCGGCTTTAGCGCG
 GAGCACTGCCAACAGAGAATCCGTGCTGGGACAAGTAGTCCGAGAGGTGATCCGCGCGCA
 GAAAGGTTATGCATCATGTGTCACAGCCTCCAAGGTGCCCATGGAATGTCTGTGGGGCT
 GTGGGCCCCAGTGCTGCGAGCCCAACCGCAGCAAGGCGGGAATACGCTTTCAGTGCACG
 CAGGGCTCTCGTTTGTGAAGAGGTGGAGAGACACTTAGAGTTCGGCTGCTCTCGGCTGTTC
CTAGCCCCCTGCCCGCTGCTGCCACCTCTCGGACTTCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTTCAGCATGAAGGAATGAAGCTGGAGAGGAAGGTAAAGAAAG
 AGAGAATATTAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRN
 AERLDLRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL
 PELLFQSTPKLTRLDSLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRI LVT SFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVC PAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPFVCDCHLKLWADLYQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYDRSRFS
 SEC FMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVT ELYLEGNHLTAVPRELSALRHLLTIDL SNNSISMLTNYTFSNM SHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTPTTHRFQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCLPFEGQR
 CEINPDDCEDNDCENNATCVDGINNVYCICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL
 DKGFSCCECVPGYSGKLCETDNDDCAHKCRHGAQCVDITINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEYGGDLCDKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGS SFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

GGATGCGAGGACGCTCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTTCGCA
GACTCAACTGAGAAGTCAAGCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTCGGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAG
GCGCGAGTCCAAATCTACACTCGTTGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAAATTACTGGGGCTTCAGCCTTGGAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGACAGCGCGAAAGCTGAAGGAGAAACCACTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAATATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCTAAACTGGAACCTGGACCCAGGATGCTTTGCGCAAC
GCCCTAGGATTTGCACTGAATGTCCAATGCCTGTGTCACTTGTCCCGTTTCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAACCTTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTGATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATGTGCTTAATTCGGGTGGACCCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
 ATAGAAAAGTTTATCCGTGAACCTTCCTTAAAGCCACCATGGGCTGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTATTAATAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT
 CCACCGAAGTGTTCACTGTCACTGTAGGGAATTTTGTGTTGCTGTCTTGTGCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRRLARRRKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

117/249

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGGCCCTCCTCTAAAGCTTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCTGTT
 TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGCAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT
 CCTAGAGAGACCTCTGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAACTTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPFVVSFWFGRRLVVS LGTVDLKQHINPNKTSDPFETMLKSLLRYSQGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWSEIGKGLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVCETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCCGTCTTTGGGCTGAAA
AAGAAAACCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCTCGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAA

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACAGGGCCGTGGCTGGAACTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLAGGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

1006172-120601

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGTGCTGCTTCGTGTTCTCGTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTACCTAAGTCCCGCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCCAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACACAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGAC**CCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGCAAGGGGTGGGCCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACAGCGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGCCGGCCGAG
 GCATGTCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGGAAGTCTTGT
 GAAACCGTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCCTGGGCGGAGGAGAGTAGGGTAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAACTGTGCGCGCCGCCGCCGCTCGTCTCTGCAGCGTGTGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGGTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCCTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGCTGTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTTACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
 GTTAACCTTGATGTTAAATGGAAAACAGTAATATCTGCGCTTTCGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTTCTGAATTTTATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACGT
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGTTCTGTAA
 AAACTTGGAATTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCACAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCGCCGAGGGAATCTTATACTTTATTGCG
 TCACTTTTAATTAATAATGATTGATAATAACCACTTTATTAATAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTTATTAAGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACCTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTTATTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAPPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFAVPRKGIYSFSF
HVIKVIQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

127/249

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCCTTACCATCGCCATCGAGCCGTTGCGTATCATCTTCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTCTGTCCTTGTGTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCCTTATTATGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTCTTTACAACCAGCGCTCCAGATAACCCTCAGGGAACCCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCTTTTTCTGAAAATCCCTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPQTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPPTVGIGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCCAACCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTCGCTCTGGGCTTGCCTCT
 TGGTGCCTCTGGTGGCCCTCGGTGCAGAGGCCATCTGGGGGTTCTGGGGCCCAAGAACCTCTCGCAGAAAGACGCCG
 AGTTTGAAGCGCACTACGTGGACAGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCTCTGTGACCC
 GCACAGGACAGAGGGCGGTGCTGTGCTGTGAACGTCCTGAACACAGAGAGAGGGGGCGCGTGTGCTGTTTGTGG
 TCCGCCCAAGAGGGCTGTGGTGTCTCTCCAGGTGCCCTAACTCCTGCGAGGGATGTTTACGCCCAAGTAACTCT
 ACCAAAAAGTGGAAACGAACCCCTGTGTGAGCCCCCACCAGAATGAGTCGGAGATTCAAGTCTTCTAGAGTGGATG
 TGTCCACCCCTGTCAACAGTCAACACCACATACAGCTCCGGGTACGCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTCAAGTCTCAATACACAGCAGCAGCACGCCCAAGTACTTCAAGTATGAGTTCCCTGAAGGCGGTGCACT
 CGTAATTGTCAAGGTGAOCTCAACAAAGGCCCTCCCTGCTCAGTCATCTCCATTCAAGATGTGGCTGTGTCTCTG
 TCTATGACCTGGACAAACAGCTAGCCCTTCATCGGCATGTACACAGCATGACCAAGAAAGCGGCCATCACCGTAC
 AGCGAAAGACTTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTCGGGGGCT
 CCTGCTCTTACCCCTTCGCAGAAAGTGAACCGGTGCATCAAGGGCACCGCCAGAAAAACCTGTGAGTGTCTGG
 TGTCTCAAGCAGTCACTGTGAGGCATACGTCAAGTGGGATGCTCTTTGCGGTGGGTATATTTCTCTCCTTTTAACT
 TGTCTGACCGTCTCTGCTGCTGCTGGGAACTGGAGGCAGAAAGAACCCCTGCTGTTGGCCATGTACCCGAG
 CCGTCCCAAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTCTCGGCAGTTCCCTTATGAGGGTTACAACAT
 ATGGCTCCTTTGAGAAATGTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTAAG
 GTTACCAAGGGCCGCTCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGCAAGAAATGTCAATTGCGACCAAGCAATACCTCTATGTGCTGAAC
 TGGCCAGGAAGGACAGCGGTGTTTCTGCGGAAAAAGTACAGATCTACCTTCTGGAACATTGGCCACATGTGGCTCT
 TCTATGCCCTTCTGTGGTGACGTGGTGTACCTACACAGACGCTGGTGAATGACAGGGAATGACAGACATCT
 GCTACTACAACTCTCTCTCGGCCACCCACTGGGCAATCGAGCGCTTCAACAACTCTCCAGCAACCTGGGGT
 ACATCTGCTGGGGCGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCAACCGGGCCCTGTGTCGCA
 ATGACCTCTGTGCGCTGGAATGGGGATCCCCAACACTTGGGCTTTTCTACGCACTGGGCACAGCCGTGATGA
 TGGAGGGGCTGCTCAGTGGCTGCTATCATGTGTGCCCACTATCAACAAATTCATGTTGACACATGCTTCATGT
 ACATGATCGCGGACTCTGACGTCTGAAGCTCTACAGAAGGGGCACCCGACATCAAGCCAGCGCCGCTACATG
 CTACAGCCTGCTGGCCATGTGCACTTCTCTCTCTGTGCTGGCGCTGGTCTTTTGGCAAGGGGACACGCGGTCT
 GGTCTGTCTTCTCCATCTTCACTCATCTGCGCACCCCTGCTCCTCAGCACGCGAGCTCTATTACATGGGCGGGTGA
 AACTGGACTCGGGATCTTCCCGGCATCCTCCAGTGCTCTACACAGACATCCTCGGCGAGTGGCGGGCGGC
 TCTACGTGGACCGCATGTTGCTGCTGGTCAATGGGCAACGTCATCAACTGGTCTGCTGGCTGCTATGGGCTTATCA
 TGGCCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCACTGCAACCTGCTCCTTTACTTTCGCTTTCTACA
 TCAATCATGAAGCTCCGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGATCGTTTGACCTCCGTGGTGT
 GGGGCTTCGCGCTCTTCTTCTTCTCCAGGACTCAGCACCTGGCAGAAAAACCCGTGACAGATCGAGGGAGCACA
 ACCGGGACTGATCCTCCTCGACTTCTTGGACGACAGACATCTGGCACTTCTCTCTCCATCGGCATTTGCTG
 GGTCTTCTGCTGTTTGTGCTGACTGGATGACGACCTGGATACTGTGAGCGGGGACAAGATCTATGTTCTTCAAG
 AGGAGCTGGGCGCTTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTTGTCTATAGACCGGTCATCTGTCTGTGCT
 GTGGGGATGAGTCCAGCACCGCTGCCAGCACTGGATGGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCCT
 GGGACAGCATGGGGTGGCATGGAACCTTGCAGCTGCCCTTCTGCCAGGAGGACGGCCTGCTCCCTGGAAACCCC
 AGATGTTTGGCCAAATTTGCTGCTTCTTCTCAGTGTGGGGCCTTCCATGGGCGCTGCTCCTTTGGCTTCACTTT
 GTCCCTTTCTAAGAGGAAGGATGAAGGGACACCTCCCCATTATGCTGCTGCATTTTGGCGCTCTCTCTCCCC
 ACAATCCCCAGCTGGGACCTAAGAGGCTCTTTTCTTCCATCTCCCATCTCCGAGGGCCTAGTCTGGGGCCGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCTGACCTGCCATTCCAGTCAAGC
 AGGATGAGTGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGTTTGGTGCTAAGGCCCTGCAAGGGG
 CCTGGGCGAGTGGCTATTCTCTTCCCTGACCTGTGCTCAGGGCTGGCTCTTACGAATGCGCTCAGGCCAATT
 TGAAGACCGCCTTCTGATTCAAGAGGCTGAATTCAGAGTCACTCTTCATCCATCAGCTCCAGACATGATGCC
 AGCAGCAGGACTGGAGGGAGAGCGCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGGCAAAACCCC
 AGCTTGTGGCTTTTCACTGCTTATGACACTGCCCAAGAAATGCCAGGGGAGGAGGATGATACAGATTGACG
 CCCTTCTGCTCTCAGACAGTGTGGGACCCCCAGTGCTTACCTTAGAAAGGGGCTCAGGAGAGGATGTGCTGTT
 CCTCTACGTGCCAGCTCTAGCCTGCTCTAGGACCCAGGCTGGCTCTTAAGTTTCCGTCAGTCTTCAAGCA
 AGTCTGTGTTAGTCATGACACACATACCTATGAACCTTGGAGTTTACAAGATGTGGCCAGGCTCTGGGAC
 CTTGGCCAGCTGGTCTGGATCCCTCTGCTCCACCTGGTCCACCCAGATGCTGAGATGGAGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGAAATGTGTTTCTCCCAAACTGTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATGAGGTGGTCTGGATCTTTCTCTCAGAGCTCTCATGCTATGGTGTGCACTTCGTTTTCTATGAATGAAT
 TGCATTCAATAAACACAGACTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLLPFYPFAEDEPVDQGHRQKTLVSLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACFESGHPVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSTYGYQGRSFEPVGTTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLARKKYQIYFWNIAITIAVFYALPVVQLVITYQTVNVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPTYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDGIFRRLHVLYTDCIRQCSCG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTCG
 ACCA**TG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCTCCAGGCTCTCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTAGGGGACTCA
 GGCAGGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTTCTGGTTCCTGCTGGTGACCA
 GGCCCTGGACCCGAGGAGGAGCAGGCAGAGTACAGCTACAGTCAACCTCGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCAGCTGAAGGATGAAATGACCAAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCTCTTCCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCTGTAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCATACCCGCACCCATGGCCAGGTACACTGGAGTGGGGTGATGT
 GCACATCACTCCCTGGAGGCCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAACTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTTCCATGGCGAGGACTATGGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCCTTCA
 GGTGAGCCCACTTTCAGGCATGTGACGCTGGGGGTGCTCCCATCCCGACAGGCCAGAA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCGATCACAGATATCAATGATCAGCCCGCTGAGTTCATCACTTCCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC
 GCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTTGGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCCCTTGGTCCCAACCCCAACCGGTGCAACGGGATTTGGCGCCTCCAGACTTCAATGGTTC
 CCATGCTACCTCACTTGGCCCTGCATTGGGTGGAGCCAGCTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC
 GTGGAGGGGACAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTCCGC
 AGTGGGCATCTTGTAGGCAACCTGGTAGCAATAGGAATCTTCCATCTCTATTTTCAACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCTGCGCCCTGAAGGGG
 ACTGTCT**TGA**ATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCACCAAGATCCAGCAGGGGACAGCAGTAGAAGAGCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGAGCAACTGGACCAAC
 TTTATGGACTGCCATGGGATGCTCCAAATGTCAAGGTGTTCGCCAAATTAATGAAGCCCCA
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 132

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLIVTRALDREEQAEYQLQVTLEMQDGHVLWGFPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEDGVEGRAQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPI SAPAGSFLLTIQPSDPI SRTLRFSLVNDSGWLCEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLTALHWPVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTLVAGIGIFLILIFTHWTMSRKKDDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTTGAGGATTAAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCAATCTCCTGGAAGCTATTACCACGAGATGGACAACATTGCCGCAGACTTTCTGAC
 CTGGCGAGGAGGTGAAGATTGGACATTCGTTTGAACCAGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAAGGCGTGAGGCGGCCGGCCGTTGGCTGAATGCAGGCATCCATTCCCAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAATGGATATTTTCTGTGGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGACAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCAGATGCC
 GAGGAACCTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTCTGTGTGCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCCTGCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGAGCATCTGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCACCTGCAGAGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTTAGGCGATGGCTCTGCTCTGCTTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCGGCGGTGCTCCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGTGCTCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTCCACCCCTGCTGGCTGGGCGGCTGCATC
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAATCATC
 TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGTTGGGCAT
 GTGGGAGACACCCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTTC
 TCGAGTCTTCTCGGAAAATATTTTCTTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTTGTGGC
 CAGGCTGGAGTGTATGGCTCGATCTTGCTCACCACAACCTCTGCCTCTCGGGTTCAAGCA
 ATTCCTCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCGCTCA
 ATTTTGTGTTTTTGTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCTCTCTTTTATAGGCTGAATACAAAGTAGAAGATCACTTTCTCTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTTGTATTACGTGTG
 ACCAGGATGGCGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCAAATTTGAGGATGGTGAAATTTATCCCATCTGTCCCTAATGGGCTTACCTCCT
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCATAACTCAT
 CTGGCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTATCCTGTGTT
 TCCTTGTCTGGTTTG
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCCTAAGTAGAGCAAGAATTCACTCAACCAGCT
 GCGCTCTGTTTCTGTTTCACTCAGCACGTACCATCTCCTTTGTTGTTGTTGTTGTTGTTT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

Signal peptide:

amino acids 1-16

FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAGACATATTTTGTCCAAAATG
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC
CCCGGCCAATGCCCCAGTGCATACCCCGCCCTTCCGCCAAGAGCACCCTGCCTCAC
AGGTGATATTCCCTCAACACCGACTTTGCCTTCGCGCTATACCGCAGGCTGGTTTTGGAGACC
CCGAGTCAGAACATCTTCTTCCTCCCTGTGAGTGCTCCACTTCCCTGGCCATGCTCTCCCT
TGGGGCCCACTCAGTCACCAAGACCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA
CACCAGAGTCTGCCATCCACCAGGGCTTCAGCACCCTGGTTCACTCACTGACTGTTCCCAGC
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCAAGGGAAGGTT
GTAGACCAATATCAAGGCCTTGACCTTCTGACGGCCATGGTTCGTGTAATCACATATTTCTT
TAAAGCCAAGTGGGAGAAGCCCTTACCTTGATATACAGAAGAAGACTTCCCATCTCTGG
TGGGCGAGCAGGTGCTGTGCAAGTCCCCATGATGCACCAAGAAAGACCTTCGTTTTGGG
GTGGATACAGAGCTGAAGTGTCTTGTGCTGAGATGGATTACAGAAGGAGATGCCGTGGCCTT
CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCCTTGTGAGCCAGAACAC
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCC
ATTTCTGCCTCTTACAATCTGGAACCCTCCTCCCGAAGATGGGCATCCAAAATGCCTTTGA
CAAAAATGCTGATTTTTCTGGAATTGCAAGAGAGACTCCCTGCAGGTTTTCTAAGCAACCC
ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGTACCACCACCAAG
TTCATAGTCCGATCGAAGGATGGTCCCTTCTACTTCACTGTCTCCTTCAATAGGACCTTCT
GATGATGATTACAAAATAAGGCCACAGACGGTATTCTCTTTCTAGGGAAGGTGGAATAATCCCA
CTAAATCTAGGTGGGAAATGGCCTGTTAACTGATGGCACAATTGCTAATGCACAAGAAATAA
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCCAAGTGGAGCTGGATTGCTG
GCAGGGATGCCACTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCCAAGTCAACAGCC
AACACCCATTAAACCCAGTCAAGTGCCTTTTCCACAAATTTCTCCAGGTAAGTAGCTTCATG
GGATGTTGCTGGGTACCATATTTCCATTCTTGGGGCTCCCAGGAATGGAAATACGCCAAC
CCAGGTTAGGCACCTCTATTGCGAATTAACAATAACACATTCAATAAAACTAAAAATATGAAT
TCAAAAAA
AAAAAA

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSIGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDIIQGLDLLTAMVLVNHIFFAKWEKPFHLEYTRKNPFPLVGEQVTVQVPMHQEQFAF
GSDTELNCFLVQM DYKGDAVFAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SVSANYLETLIPKMGIQNAFDKNADFSGIAKRQDSLVQSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVFNRTFLMMITNKATDGLIFLQKVENPTKS

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCG
 CTGAGTCCAAGATTCTTCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGGAAGCACCAG
 CCTTTATCTCTTACCTTCAAGTCCCCTTTCTCAAGAACTCCTTGTTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCAATCTCAGGGTCCA
 GCGTACCTCTCAATGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTTCCA
 TGGGGGTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACACCTCCAATGGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAAC
 CTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGC
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
 TGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTAGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT
 TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACAACTTCCCATAGTGCATCTACTCGAGTGAAGTGAAGCAA
 AGCCTGGTGGGTCCCTGGTGGCTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCG
 GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
 CTTTAACACAGCTGTCTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGGCCCCACAGGCCAGGTGGAGTCCCTAACTGGTTCTGGAGGAGACCAAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTTGAGCAGCCCCGAAGCAAG
 TGCCGATCTTCTAGGAAGGAAGAGACCTGGGCACCCAGACCTGGTTTCTTTCTATTCTATC
 CCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTTCACC
 TTTCTTGCCCTTACCAGACACTGGAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCTAACACACAGGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG
 CTCTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGTGACTCCATCTGGCATTCAAAAA
 TCTCCAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSA NTGSSVSSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSI VTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE
 SSTPSSGASTVTNNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
 SNGAGTATNSESSTTSSGASTATNSDSTVSSGASTATNSESSTTSSGASTATNSESSTSS
 GASTATNSDSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSTTSSEAST
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVA VGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
 GPGGNHGA PHRPWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGCGCTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTGCGCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAG
REVEKVFNGLSNMGSHGKELDKGVQGLNHGMDKVAHEINHIGQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

TCCGGGTGCCAGGGGGCTCCGGCGGGCGGGGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGCG
 CGCGGGGGGCGACTGACGCTGGCTGACCTGACTCACTCAGGTCCGGAGGGGGGGGGCCCCGGGGCGACTCG
 GGGGGGACGCCGGGGCGGAGCTGCCGCCGCTGAGTCCGGCGAGCCCACTGAGCCCGAGCCGCCGGACACTGCT
 GCTCGTGCTGCTGG**GAATGCT**GGCAGCCGATGGGCGCTGAGAGCACTGGCTGCCGCCCTGGGGCGCGCTGGCG
 CCTCGGCGACCGCTGCTGCTGCTCTGCTGCTCTGCTCTGCTGACGGCCGCTCCGACACTGGGCGCTCAGC
 CCGGGACTCAGCCTGGCTCTGGGCTCTGAGAGAGGGCACTCTCAGATTGCAAGTGCACACATCTCCAATCA
 ACAGCGCTTCTGCTGACAGGAGTGCAGAGCACTCTACGTGGGTCTCGAGAGGCCCTCTTTGGCACTCAGTAGC
 AACTCTCACTTCTGCCAGCGGGGAGTACAGAGAGCTGCTTTGGGTTGCAGCGCAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGGCAAGGACCCACAGCGGAGCTGTCAAATCATCAGATGCTCTCTCGGCTCAGCGGCAGTCT
 CTGTTCACTCTGGCACAGCAGCTTCAGGCCGATGTGATCTCACTCAACTGAGAACCTTCACTCTGGGAGG
 CACGAGAAGGGAACTGTCTCTGGAAGTGGCAGGGCGGCTGCTGCTTGCACCGAAATTTCAAGTCTCAGCTGCG
 TTGGTGGTTGATGCGGAGCTCTACATCTGGAACATCAGCAGCTTCAAGGAATGACCGCCGCACTCTCGGAGGCG
 CAAAGCCTTTCGCCCCACAGAGCAGAGAGCTCCTCAACTGGTGCAAGAACCAAGTTTGTGTGGCTCTCAGCTAC
 ATTTCTGAGAGCGCTGGGACGATGCAAGGCGATGATGACAGATCAATTTTCTGAGCGAGACTGGCCAGGAA
 TTGTAGGTTCTTTGAGAACCAATTTGTCCGCAATTGCCGCATCTGCAAGGGGGCATGAGGAGTGGAGAGCGGGT
 CTACAGCAGCGCTGGACCTCTCTCTCAAGGCCAGCTGTGCTGTCAGCGCCGACGAGCTGCTCCCTTCAACT
 GTGCTGCAAGATGTCTTACGCTGAGGCCGCCCGAGGATGGGTGACACCTTTTCTGTGGGTTCTTCACT
 TCCGAGTGGCAGAGGGAATACAGAGGCTCTCGGCTCTGTGTTCTTCAAAATGAAGGATGTGACAGAGACTTTC
 AGCGGCTCTACAAGAGGTGAACGTTGGAGACAGCAGTGGTACACGTCAGCCACCGGTGCCCAACCGCGGCG
 CTGGAAGCTGCATCAACCACAGTATGCCGGGAAGGAGAACTCAACTCTCTCTGAGCTCCAGACCGCGGTGCTG
 AACTTCTTCAAGAGCACTTCTGATGAGCGGGGAGCTCGAAGCGCATCTGCTGCTGACCGCCAGGCTCGC
 TACAGCGGCTGGGCTGTACACCGCTGCCCTGGCTGACACACATCAGATGCTCTCTCTGGGCACTGTGACG
 GCGGCGCTCCACAGAGTCACTGAGCTGAGCTGGGCGCCGGGTGGCATCTGAGAGTCGACATCTTCTCATGAG
 CAGCCCGCTGCAGAAATGTCTCTGGCAGCAGCGGGGGCTGCTGTATCGGCGCTCACACTCGGGGCTAGTGTCCAG
 TCGCCATCTGGCCAACTCGAGCTGTACCGAGCTGTGGGAGTGGCTGCTCGCGCGGAGCCCTCACTGTGCTGG
 GCGGCGTCCAGCTGCGAGCACTGACCTTACAGCGCTCAGGTGGCCACAGCGCGCTGATCCAGGACATCTGAG
 GGAGCCAGCGCCAAAGCACTTTCAGCGGCTGTCTGGTTGTGCCCGCTCTTTGTACCAAGGGGGAAGCAACA
 TGTGGCAAGTTCAGTTTCAGGCCCCACACACAGTGAACACTTTGGCTTGGCCGCTCTCTTCAACATCGCCGACCGA
 CTCTGAGTACGCAACGGGGCGGCGGCTAACTGGCTGGCCCTGGCATGCGCTCTACCACTGGGGAGCTGTGCTGTG
 GTGGCGCCACCAACAGCTGGGGAGTTCAGCTGTGCTGTGCTACGAGAGGGGCTTCCAGCACTGGTAGGAGCACTAC
 TGGCCAGAGTGTGGAGGACGGGGTGGCAGACCAAAAGATGAGGTGGGAGTGTACCGTCAATTTATCAGACA
 TCGGCTGTGCTGACCACTGTGGTGGCAAGCCAGCTGGGGTCAGACAGGCTCTCTACGGAAGGAGTTTCGTTGGT
 ATGTGCAAGCTCTTTTGTGTCGGCTGCTGCTCCAGTTTATTTCTGCTTACCGGACCGGAACAGACATGAAA
 GTCTTCTTCAAGAGCGGGAATGTGCAAGCTGTCAACCGAGACTGCGCTTGTGTCGCTGCCCTCTGAGACCGCG
 CCACTCAACGCGCTAGGGCCCCATAGACCCGCTGATACACGAGSGTACAGTCCGTGTACAGACGCCCCCG
 GGGGCGGGAGTCTTCACTAGTCAGAGAAGGAGCACTCAGCATCAGACAGACTCTGTTGGAGGTTATCCCAAGT
 TCGCCCGCGCGGGTGCGCTTGGCTGGAGATCCGTGACTCTGTGGT**TCGAG**AGCTGACTTCCAGAGAGCG
 TGGCCTGGCTTCAGGGGGTGTGAATGCTGGAGAGGAGTCAACTGGAACCTCCCTTCCGCTGCTCTGTGTTGGAAAC
 AGCACGCTGTGTGGCGGGCTTGTGGAGGCTTGTGAGCAAGTGGCTGCTGCTCTCAGTACAGTAGGACAGCACTC
 TACACCCAGACACCCAAACAGCGCTGGCCCGAGAGTCTGTGCCAAATATGGGGGGCTGCTAGGTTGTGTGAA
 CAGTGGCTCCTTATGTAAATCAGGCTTTTGTTTAAAAACAAATCAAATGTGAAATAGAACTGAGGGGAAGAG
 ATAGATCAGAGATCGACGACACACGGCTGCTCCAGTTCTATGGCTTCCAGGGGATCTGGGAGTGCATCCAAATGG
 TTGCTGAGACAGATTTGAAACACTCACCACTGGGCTCTTCACTTCCAATTTCTCCGCTGACCCGGCTGCG
 CTGTCTCACTGAGATCAGGACCACTTGGGCTGGTGCTTCTGCTTCTCGAGTCAGCCGAGGATGTAGTTG
 TTGCTGCGCTGTCCCAACACTCAGGACACGGGCGAGGCTAGGTTGGCATCGCGCGCTCCAGAGTCTCAGAGTCTGGGCT
 GTTCCGCACTCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACAGGAGACAGGCGAGCTCAGGAGAAGA
 TTTCTGACAAATGTAGCCCTTTCTCGTAAGTACAGGAAGACACTGCTCGCTGCTTCTGCTGTGTGGTGA
 GAACCCGCTGTGCGCCCTTCCACCACTTACACCTCGCTTCATCTTTGAAGTCAAAACAGGAGAACTCACTGCAC
 CTGGTCTCTCCCGAGTCCCAAGTTCACCTTCATCGCTCACTTCTCACTTCAAGGATATCAACACTGAGTCCG
 AGCAGAGGGGCGGTAATTTGATGTGGTTTTATACATTTTATAAGATGCATTTTATGTCAATTTTATAATAA
 GTCTGAAGAATTACTGTTTAAAAAATAAAAA

FIGURE 142

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLQPPPTWALSFRISLPLGSEERPFPLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFSETGQEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFKDHFLLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDRHLKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVS LYQP
QLATREPWIDIEGASAKDLCASSVSPSFVPTGEKPEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGTLGQGEFQCSLEEGFQQLVASYCPVVEDGVADQ
TDEGGSVPIISTSRVSAPAGGKASWGADRSYWKFLVMCTFLVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPVRVLGSEIRDSVV

```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGAGGAGTGTGCAGCTGCGGGCGGCGCGCGGCTACGAAGAGGACGGGAGCAGGGCGCGTGCAGACCGA
 GCGCCAGCCGCGGAGGAGCGGGGAGGCGGGAGCGCCGCGACCTCGCGCCGAGCGCCGCTAGCGCGCGC
 TCCCGCCCGGCTCCCGCGCGGAGCGGAGCGCGCGCGACCTCGCGCCGAGCGCCGCTAGCGCGCGC
 CGGGCATTGGTCCCTCTTAAAGGCGACGGGCGCGCGCGGGGGGGTGTGCGGAACAAAGCGCGCGCGGGG
 CTTGGGGCGGCTCGGGGGCGCGATGGGCGGGCGCGCGCGCGCGCGCGCGCGCTCCCGCGCGCGGCTCG
 CGCGCGTAGGGCGGGCTGGCCTCGTGGGCGGGGCGACGGGGCTGAGGGCGCGCGGAGCGCTCGGGCGCGGGG
 GGGCGGGCGCGCGCGCGCGGGGCGGAGCGCGCGGGGCATGGCCGCGCGCGCGCGCGCGCTGGCTTCAGGTGC
 TGTCTGGGCTCGTCTGGGCTTCGTGCTGGCTCGCGGCTCGTCTGCCCCGGGCTTCGAGATGAAGCGAGCGG
 GCGCCACCGGCGCGCGACCGCCGAGGGGCTGCCGCTCGGGCAGGCGCGCGCTCCGAGGCCGCGGGCGCGCG
 GCGATCGCGCGGGGCGAGCTCTGGCCGCCGGCTCGGACCAGATGGCGGGCCGCGCGACAGGAATTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGCTGGCGCCTACAGAACATGGTCCAGACAA
 TTCTCGGAAAGTTCAAGTTCTTCAAGTGAGGGTTCTGCACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGAGACTCTACCGCGCCCGAGAAGTCTCTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTATAGAGCAGATGATGACGTGATCATCAAGAGAGACCGCTCGGAGAACTTCTCGAGGAGTT
 TGAACAGCAGCGAGCGCCCTCTTTCTGGGCAGACAGGCTGGGACCCACGGAAGAAATGGGAAACTGGCCCTGG
 AGCCTGGTGAAGTTCTGCATGGGGGGGCTGGCGTGATCATGAGCGGGAGGTGCTTCGGAGAAATGGTGGCGC
 ACATTTGGCAAGTGTCTCCGGGAGATGACACCACTGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
 CAGGGGTGCGAGTGTCTGGCTTATGAGATGCGGCAGCTTTTTATGAGAAATACGAGCAGACAAAGAGGGGT
 TCAATAGAGATTCCTATACAGTAATAAATTCACCAAGCTATACATTTACACCCCAAAACAAACCCCTACGACT
 ACAGGCTCCCAAGCTACATGCTGAGCGCAGAGATATCCGAGCTCGGCGCATCGCAACATACAGCTGCACCGGAAA
 TTGTCGTGATGAGCAATATCAACACACAGAAATTCACAAAGAGACCTCCAGCTGGAAATCCCTCCCTCTTCA
 TGAGGTTTCAGCCGCCGCGAGCAGAGAGATTTCTGGAATGGGAGTTTCGTACTGGAAATACTGTATTCGGCAG
 TTGAGCGGCAGCCCTCTCGAAGGACGTCGACTCCGCCAGAGGGAAGCCTGGAGCGACATTTGATTCGAGCTCA
 TGGAGATGATCAATGCCACAGCCGAAGCCAGAGGGCGCATCATGACTTCAAGACATCCAGTAGCGGCTACCGCG
 GGGTGAAACCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTGTGTAACAAAGACAAAGAGGAAACAA
 TGACGCTCCCTGTGAGAGGCGACCGGTATTTACAGCAGACTTCACGACAAATCCAGTTTGTGGAGCATGAGAGC
 TGGATGCACAGAGTTTGGCCAGAGGAATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACTCCCTGAAGA
 AGCTCGTCCCTCTCAGCTCCCTGGGTGCGAAGAGTGAGCACAAAGACCAAGATGATTCAGATCACTGA
 TTCCTTTGTCTGGGCGGTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAGACGCTGTCTTATCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCGACTCCAACCTGACAAAGGCCAAACAAAGTTGAATGATGA
 GAGATTAACGCATTAAGTACCTTAAGCCGACATGCAGATTTTGGCTGTGTCTGGAGAGTTTCCAGAGCCCTGG
 CCTTGAAGTAGGATCTCCAGTTTAAACATGAATCTTTGCTCTCTCTCTGGCGAGCTCGACTCGTGTGTTTACTA
 CAGAAITCTCTCAGCGATGTCGAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCCAACTCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCCAAGTGACACCAATTTTGGCTTTACTCAGAAAACTGGCTTCT
 GGAGAAATATGGGTTTGGCATCAGCTGTATTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGGCTGGGAGATGTGAACCTTTCAACAAGGTTTCCAGGCGGTTTGAAGAGCTTTTAGGAGCC
 AGGAAGTGAAGGATAGTCCAGTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAATGT
 GCTTGGGTCCTAAAGCATCGAATATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTTGTGGAAAAAGACGTTTT
 TAAATTTCTAATTTATTTTCAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATAACAGGATATATTATAC
 AAGTGGTTTTCTTACATAGGACTCTTTAAGATTGAGCTTTCTGAACAAAGAGGTGATCAGTTGTGCTTTGAA
 CACATCTCTTGTGAACATTTATGACGACACCTGCTTAACCTTTGACTTGAATGTACCTGATGAACAAACATCT
 TTTAAAAAATGTTTTCTTTTGAACCTTTGCTCCAGTCTATGGCAGAAAAAGTGAACATTCCTGCAAGATAT
 TATTTGTAACAAACACGTAACTCTGGTAAATGTTCTGTGTGATTTGAACATTTCCAAGATTTCACTTTTGT
 GTTTTGTTTTTTTTTTACAATTTGTTTAAAGCCATTTCATGTTCCAGTTTGAAGATAAGGAAATGTGATATA
 GCTGTTTCACTATTGTCCTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCTGCTCGCATGCTGGC
 CAGTAGGTTTTTTTTGTTTGTGTTTTGTTCTTTTTTGAAGCAGGATCTCACTCTGTATACCAGCGCTGGAATG
 CAGTGGCGAATCTTGGCTCACTTTTAAACCTCCACTTCCCTGGTTCAAGCAATCCCTGCTTTGCTCCCTCGCT
 AGCTGGGATTCAGCCACACACCCACCCAGCCAGNAGTTTTTTGATTTTTAGTAGAGCGGGGTTTACCAT
 CGAAGCCAGCTGCGGACGTAGGTTTTTAAAGCAGGGGCGTGAAGAGGCACAGTAGGATGTGGCTGTGTTCTCG
 TGGTAGTTTCTTGGCGCTAAATAGACCTGGCAATTAATTTCAAGAAGGATTTGGCATTTCTCTCTTGACCTTT
 CTCTTTTAAAGGTAAAAATTAATGTTTGAATGACAAAGATTAATTAACATAAATCTGATGTACACAGACT
 GAACATACACACATACACCTTAATCAAAACGTTGGGGAATAATGTATTTGGTTTTGTTCTTCTCATCTGCTGT
 TGTATTGGGTGGAGATGTTTTCTTCTTCTTATTACTGTTTGTGTTTATCGTTTGTATCTGTAATACCTTTAA
 TTTATTTAAATCTGTTGTTTCAGACTCTGCCATTTCTGAGTACCTGTTAGTTAGTATTATTATGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTCAGTAAACCGATCTCCAAAGATTTCTTTTTGGAACGCTTTTTCCCTCC

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTGGG
GACAAAGTGAANTGAATCTGTCATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAATAAG
CCTGATGCTCATTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTGAACCATTTTGTCTCATT
ATTCCTGTTTGTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAAAGTTAAACACGAAAAAA

FIGURE 144

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKINILIPLSGRFDMFVRFMGNFECTC
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPNDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKKVVQAGLKTFRSQEVGVVH
VHHVPVFCDPNLPKQYKMC LGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

GGACAACCGTGTGCTGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTTCGCATGGCAGAGTGCT
ACGGACGACGCGCTTATGAAGGCCCTTAGTCCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACCGGAAAGTACCCC
ATTCTGGTCGATCAAAACCAACAATGTTCCATTGTTTGTGATCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCGCGGAGCCAGCTGCAAAAACAACTGAGGACCCATAAGTG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACTCTATACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCTCAGCTCT
CAGGTGAAACTGCGATAGAAAAACCCGAAGGTTTGGAAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCAGTTATTGGCA
GTAGGACGAAACAAGTAATAAAATTTGATGACATCGAAACGTGTTATTACATGCTGTGTAATTC
TAGATCTAAACTCTATGAATATTTAGATATTTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTTCAATACATTTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAAAATTTTAAACCTACTTGATATTTCCATAACAAGCTGA
TTTAAGCAAACATGCATTTTGTTCACAGGAGAAATATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCCTAAAAACCTAATTTAAAAATAAAATTTTGGTTCAGGAAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPVSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPIS ETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAE EPIYENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDD IETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

148/249

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGGGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAAGTGAAGTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGC
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCACTTCCAGATTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAGGTTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGTGAGCAGAGTCAAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGAAAAATCCA
 GCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAG
 AAAATGTAGGGTGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC
 ATTCAATCCCCATTTATCAGCCTCCCCCAGCACCCCTCCTACACGATAGGGGTCTTCC
 TGGACTATGAGGGTGGGACATCTCCTTCTCAATACAAATGACCACTCCCTTATTTTATACC
 CTGCTGACATGTGAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTATATGTCCAGTGTCCCTGGGGATGAGACAGAGAAAGCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTTCTTCTGCCTGAGCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGAGCGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTAATCATGCTTGCAGGTTTGAGGGCACAGTGTTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTATTCCACATTAATTTACTTTTTCTCTA
 TACCAATACCCATGGAATAGTTATGAAACACCTGCTTTGTGAGGCTCAAAGATAAAGAG
 GAGGTAGGATTTTCTACTGATTCTATAAGCCACGATACCTGATACCAAAACAGGCAAG
 AAAACAGAAAGAGGAAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTTAAACAAATTAACATAACAAATATATTTAAAGATGATATATACTACT
 CAGTGTGGTTTGTGCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGGTGTAATT
 CAGCACATTAATAAAGTAAAAAGAAAAACCATAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYGVGCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPIYQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCT
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCAATTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAGAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTGTGATTGTAGATTCTACTCTACTGAGGATCCTGAAACTGTAG
 ATAAATTTGTTCAACTTGTTTTACATGAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACCAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTACAACATATAA
 GAACCTTGCAGATGGACTGCTTCCCTTTGGAGTAACAATAAAACCTTCGAAATGAACGGG
 GTCTCCGAGAATAATTTGCCATGAAATAACAAACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTTCAAGTGTG
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCAGGACTGGATTACTTCAAAACTGGTATCTA
AGAGACAAAGCCTCATGGAACAGATAACATTTTTTTTGGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGTCTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTGTGAGAAATTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTCAAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCTATTATGAAAGGTCAAGCAAAGACAGCAGAAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

GTCTGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTTGGGGATCCCTCAGCCTAACACCCACAGACGTGACGTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGCGTGGCCGCCTTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGGCCGGCGGCCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCTACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAATGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCGTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCTCAGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGCAGCCGCCTTGGCGGTGCCGCCAACCCCCGCACCTCTGGTCCACGC
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGAGGGGCGCTCTGA
AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAGAGGAAAAACCGCTGCCTCCAGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCACTGTTCTCAGGACTAGACGCTGTTTAGTCCGGTACTT
GGCGCTTTGTTTCTCGCTGAGGTTCTGGGAAGGAATAGAGAGGGGGCCCCAATTTTTTTTA
AGCGGCCAGATAATAATAATGTAACTTTTGGGTTAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAPQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHVAAGVGTALALLSCAALVWHFCLDRWGCPRRRAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

AGAGAAAGAACGCTCCACAGCTGAAGCCAAATGCAGCCCTCCGGCTCTCCGGAAGAAAGTCC
CTCCGCGGATGAGCCCCCGCGTGCCTCCCGCAATATCCCAAGCGCGGTGGGGCAGCGGG
CCGACGCCGACAGATCGTCGCGTTTGGCCCTGGGAGTAGGATGTGTGAAAGGATGGGG
TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATTCGGTAGAGTCTCGCGCTGCTGCT
CTACGGCCCTCAATCTGCTCTTTGGTTAAATGTCATCATGTGTGGCAGTTTCTGCTTGA
TGAGGGACTACCTAAATAATGTCTCACTTTAACTGCAGAAACAGGGTAGAGGAAGCAGTC
ATTTTGACTTACTTCTGTGTGCTTCATCCGTCATGATGCTGTCTTGTCTGTCTTCTATCAT
TGTGGGATGTGTAGATATATGTGGAACGGTGAAGAAATCTGTGCTCTCTGATGGTACT
TTGGAAGTTTGTCTGTCAATTTCTGTGTAGAACATGGCTGTGTGGCGTTTGGACATATGAACAG
GAATCTATGTTTCCAGTAAATGGTCAGATATGGTCACTTTGAAGCCAGGATGACAAATTT
TGGATTACCTAGATATCGGTGCTCTCATGCTTGGAAATTTTTCAGAGAGAGTTAAAGT
GCTGTGGAGTAGATATATTTCACTCATGGTTGGAAATACAGACAGATGGACTGGCCCCAGAT
TCCCTGCTGTGTTAGAGAATTTCCAGAGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTGGAGGAACCAACAACATGC
AGGTGCTGAGGTTTCTGGGAATCTCCATTTGGGGTGCAGCAAAATCCGCGCATGATCTCAC
ATTACTCTGCTCTGGGCTCTGATTATGATAGAAGGGAGCCTGGGACAGACCAAAATGATGTC
CTTGAAGATATCAACACTCAGCAGCTGTCAATGTCCCTCAGTAGAATCTGTTGAAACCAAGCC
TGTCAGAAATCTTTGAACACATCCATGGCAACAGCTTAAATACACATCTTGATAGTGAG
GAGTTATAAAGAAAGATGTCACAGAAGAAACACCAAGCTTTTATTTGAGCTTGTGAAT
TTTGAGTACATATCTATGTTTTCAGAAAATATGAGAAATAAAATGTTGCCATAAAATACAC
CCTAGCATATACATTTCTATGCTTTTAAATAGGATGGAAGTTTATGTCATAGTCAC
CACCTGGACAAATAATTTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
CTGTGTATGACTTTTACGAACAGAGTTATGTTTGGAGCAGCATGGTTTGTATTAGCATTT
CGCATCCATGCAACAGGAGTCACATATGGTGGGACTGGACCATGTAAGGTTGATTACTT
CTCCAACCTAGTATATAAAGTACATTAATTAATGCTAACATAGAAGATGTAGAAAATCTAATA
ACTTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAAAATATATATCAGAAAATCTT
AATATTGGTGACTACCTAAATGTGATTTTGGCTGGTTACTAAAAATATTCTTACCCTTAAAA
GAGCAAGCTATACACATTTGCTTTAAGCTGATCAGGGATTTTGTATATAAGTCTGTGTTAAA
TCTGTATAAATCAGTCGATTTAGCTGTGATAATGTGAAGATAACCATATGAAAGGAAA
ATTTGCTCGTATAGCATCATTTATTTAGCCTTTCCGTTTAAAGCTTTACTATTCTGT
CTTGGGCTTATATACACATATACTGTTATTTTAAATACCTTAACCACTAATTTGAAATTA
CCAGTGTGATACATAGGAATCATTTATCAGAAATGTAGTCTGGTCTTTAGGAAGTATATAAA
GAAAATTTGCACATAACTTGTGATTTCAGAAAGGACTGTATGCTGTTTTCTCCCAATG
AAGACTCTTTTGAACATAAACACTTTTTAAAAAGCTTATCTTGGCTCTCCAAACAGAA
GCAATAGTCTCAAGTCAATATAAATCTACAGAAAATAGTGTCTTTTTCTCCAGAAAAT
GCTTGTGAGAATCAATAAACATGTGACATTTAGAGATCTTGTGTTTATTCTCAGTATTA
ATATACTGTGGCAAATTCACAGATTAATAATTTTTACAAGAGTATAGTATATTAATTT
GAAATGGGAAGTGCAATTTTACTGTATTTTGFTATTTGTTTATTTCTCAGAATATGGAA
AGAAAATTAAGATGTGTCATAAATATTTCTCAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

AAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCC
 TGCCTCGGGCCTCCTCCAGCCAGTGTCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATACAGAGCCAGCAATGTTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAG
 TGATTCTGGATAAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTGTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGATCGGGAAGCTCAAGTGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTCCCTGTGGGAAGAGCTCGAAGACCCCCGT
 GTGTGGTGGTGGGGAGGAGGCCTCTGTGGATTCTGCTGGCCTTGGCAGGTGAGATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCTCTGAGACCCCACTGGGTCTTCAGGCAGCCACT
 GCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAGAGTATCATCATTTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCCTCAGTCCA
 GGTCAATTGACAGCACACGTTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACATG
 TCTGGAAGGCTGAGCTGTTAATTGCTGCTGCCCTTTGCAAGTGTGGGAGCCGCTTCTTCTCTG
 CCCTGCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTTGGGTACACC
 CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCTCTGTAAGAGACC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCC
 AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
 CTAGAGCAAGAACCAGTTGTAATATAAAATGCAGTCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCACTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAATAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNRSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCVGGSGILDPHWVLTAAHCFRKHTDV
FNWVKRAGSDKLGSPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCCQDGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGCGTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATATGGCCCTCCAGCCCTGGGCTGACCCCTGGAGCCTCTCGGGCC
 TTTTCTCTTCCAACCTGCTTCAGTGCTGTGCCGACGACAGCCGGGGGAGGCGGGCAGGGGCCCATGCCCA
 GGGTCAGATACTATTCAGGGGATGAACGTAGGGCACTTAGCTTCTCCACCAAGGGGCTCCAGGATTTTGACA
 CTCTGTCTCTGAGTGGTGATGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTA
 AGAAGAGAGCAATGAGACACAGTGTTCACACTCATCCGTGTCTGTGTTCTTACAAATGTACCCATCTCTACA
 CCTGCGGCACCTTCGCTTCAGCCCTGCTGTGACCTTCATTGAACCTCAAGATTCTTACCTGTTGCCCATCTCGG
 AGGACAAGGTCTATGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGTCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACCTCTGGGCACTGAGCCCATCTGATGCGCACACTGGGATCCAGC
 CTGTCTCTAAGACCGACAACCTCTCCGCTGGCTGCATCATGACGCTCCTTTGCGGAGCCATCCCTTCGACCC
 AGGTCGTCTACTTCTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGCTGCGCAAGTAAGTACGTGGGCGGCAAGAGCTGCTGCAGAGAAGTGACACCTTCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCTATCCGCGCACGCGCTCTGCTCCCGCCATTCTCCCA
 CAGTCCCCACATCTACGCACTCTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTCGGTTTGTGCT
 TCTCTCTCTTGACATTGAACGTGTCTTAAAGGGAAATACAAGAGTTGAACAAGAAACTTCACGCTGGACTA
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCACTGCTGCTGAGTGGGCCCCCTCTCTGATAAGGCCCTGACCT
 TCAAGAGGACCACTTCTGATGGATGAGCAAGTGGTGGGACGCCCCCTGCTGGTGAATCTGGCGTGGAGTATA
 CACGGCTGCACTGGAGACAGCCAGGGCCTTGATGGGACAGCCATCTTGTCTGATGACCTGGGAACCCACAG
 GGTGCTCCACAAGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTGTTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGGCCCTGAGACCTGCGCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTGGCCGGGACCCCACTGCTC
 GGGACCTGAGTCCGAAACCTGTTGCCTCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGCGCTCAGAGCCGCCGCAAACTATTA
 AAGAAGTCTGGCTGTCCCAACTCCATCTGGAGCTCCCTGCCCACTGTCACTCTGGCTCTTATTATT
 GGAGTCATGGCCAGCAGCATCCCAAGCCTCTTCACTGTCTACAATGGCTCTTGTCTGCTATGATAGTCAGG
 ATGAGATTTGGGGTCTCTACCAAGTGGGCACTGGAATGGCTTTATACCTGTGATCTCTGCTACTGAGTGGTGG
 ACAGCCAGGACAGACCTTGGCCCTGGATCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGTCCCGTGA
 CCAGGTGAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCACTTTGTCACTGTCACTGTCTCT
 TTGCTTAGTGCTTTCAGGAGCCCTCATCATCTCGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG
 TTCAGGGCTGTGAGACCTGCGCTTGGGGAGAGGCCCGTTAAGCAGAGAGCAACACTCTCCCTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGCTCGCGTGCAGGCACCTGGCCATGTGGCTGGCGGGCCCAAGCAGAGCCCTGACTAGGATGACAG
 CAGCACAAGAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCACTGATGACACTCAGCAGGGT
 ATGCACAGCACTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
 CCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGATCTTCACTGTGCGCATTCAGGACCCCTC
 CAGAAACACAGTGTTCAGAGACCTAAAAAACCTGCCTGTCCAGGACCTTATGTAATGAACACCAACATC
 TAAACATCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCATGAGGAGTGTCTCCCTCTGCTTCCCTTACCAGTCTGTCACCGCTGACTCCAGGAAGT
 TTTCTGAAGTCTGACCACTTCTCTTCTGCTTCAGTGGGGCAGCACTGATCCCTTCTGCCCTGGCAGCAATGG
 CAGGGTAACTGAGCCTTCTCACTCCTTTACCCTAGCTGACCCCTTCACTCTCCCTCCCTTTCTCTTGT
 TTTGGGATTGAGAACTGCTGTGACAGACTGTTTATTTTATTAATAATATAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVYGAREAILALDIQDPGVPRCLKNMIPWPASDRKKSECAFKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKQSPFDPAAHKHTA
VLVDGMLYSGTMNNFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDA SFVAAIPSTQVVYFFFE
ETASEFDFFERLHTRSARVAVCKNDVGGKLLQKKWTTFLKAQQLLCTQPGQLPFNVIRHAVLL
PADSPTAPIYAVFTSQVQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEETQLFPDPEPVRNLQLAPTQGA VFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNISILELPCPHLSALASYWWSHGPAAPVEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYVWDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLVSGALIILVASPLRALRARGKVQCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

AGGGTCCCTTAGCGCGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG
TGAGC**AT**GGCTGGGCGAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCT
TCAGAGGCTGCCAAAACCTGACAATATCTACAGTAGGTTGGAAGCCATTATCTACTGATGGA
CCGGGTTTCTCAGATCTTTCAGATACACGGTCAATAATGTACACCATGCTTAACCCAAAAGAG
GTCCTTTTATGCGCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA
CCTGAAGATCATCAAAGAGAAATTTAAAAAGAGTTTGTATTTCTTCTGGAAGAAACCTTAGG
TGGCAGAGGAAAATTTGAAAACCTTATAAATGTCTTAGAATACTTGGCGTTGCGATGCGAGT
ATTTTTTAAATAGAAAGATATCATGGATTCTTTAAAGAATGAGAATCTGCAGTGGTGAT
TTTGAAACTTTTGACTACTGTCTTTCTTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
CATCTPTTCCACCTTCATTCGGGCTCTTTTGGAAATTTGGGCTACCAATCCCTGTGCTTATGTTCT
CAGTATTCGGTTCCCTGCTGACTGATCACATGGACTCTGGGGCCGAGTGAAGAATTTCTTG
ATGTTCTTTAGTTTCTGCGAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
GGAACATTTACAGAAAGGCTCTAGGCCAGCTTTTGCTCATCTTCTACTGAAAGCAGAGTTGTT
GGTCTATTAACTCTGACTTTTGCTTTGATTTTGTCTGACCTCTGCTTCCCAAGCTGTTTAT
GTTGGAGGCTTGATGAAAAACCTATTAAACCAAGTACCACAAGACTTGGAGAACTTCATGTC
CAAGTTTGGGACCTTGTTTGTCTTTGACCTTGGGCTCCATGGTGAACACCTGTGAGA
ATCCGGAATCTTCAAGGAGATGAACAAATGCCTTTGTCTACCTTACCCCAAGGGGTGATATGG
AAGTGTCACTGTTCTCATCTGGCCCAAAGATGTACCACTGGCTGCAATTTGAAATTTGGGA
CTGGCTTCTCAGATGACCTCTGGCTTACCCAAAGCATCCGTCTGTTTGTGTCACCCACAGTGC
GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
AGAGCAGCGCTGAAAACATGTGTCGAGTAGAAGCAAAAAGTTTGGTGTTCATTACAGT
AAAAGAGCTCAAGGCAGAGACATGGCTCTTAAGATGAACAAATCATGGAAGACAAGAGAT
ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTATCTCGCGCTCCCACCCGCTCAGCCCCACAG
CGACTGGTGGGCTGGATTGACCAGCTCTCCAGACAGGGGGCGCGACGCACTCAAGCCCTA
TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACAGTTTGTGTTTCTGCTGGGGC
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCTCATGTTGCTGGTGGCTGCGT
TGCCGCGAGAAGGTGAAGGACAT**TA**AGGCCAGGTGCAAGCTTGGCGGGTCTGTTTGGTGT
GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGGCCCATTTCTCTAGTCTTTC
TAGTTATCTCCTGTCTTTCTTGAAGAAGAGAAAATGGCCAAAATCATCTTTCCACTTGTG
TAATTTTGCTACAAATTCATCCTTACTAGCTCTGCGCTGCTAGCAGAAATCTTCCAGTCCCT
CTTGTCTCTCTTTGTTTGCCATCAGCAAGGCTATGCTGTGATTCTGTCTCTGATGACTTG
GACCACATGACCTCAGATTTCCAGCCTTAAAAATCCACCTTCTCTCTCATCGCCTCTCGGAA
TCACACCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTACCTCTGCCCC
TATATCTCATATGGAATAACATCAAGAAAGACACCTTGATATTTCTTCAGTTTCTGTGTT
TGTTCTCCACATATTTCTTCAA**GT**CTCAGGAAGCTTGCCCTGTGCTGTAGAGTTCTAGGGC
CGGACACAGGCTCACAGGCTTCCACATTTGGGTCCCTGTCTCTGGTGCCACAGTGAAGTCTCT
TCTTGGCTGAGCAGCAATGGAGACTGTAGTTCTCAGATTTCTGAAAAATAAAAGTTTACA
GCGTTATCTCTCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKGKRP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGLSEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF
INSDFAFDFAFRLPLPNTVYVGGLEMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVVGIPVFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFPQWHEQYLFDFVFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

GGGCTGTGTTGATTTGTGGGGATTTTGAAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCCTCGGCATGTCACACACCTCACACATTCTGTCCACACCCGTCACACACACATACCATTGTT
TCCATATCCCCCAGGTCACGCCCTCAGTGGTGTCCATCAGCAGGGCATACCTGAAGCTCT
GGGTGCAGCCCTCCGTCAGGTGGGACGGCGGCTTCATCCCTCCTTTCTCTCCAAAGCCCA
ACTGCTGTCACTGATCTCTGCCAAGGAGGAGGAACTCGAGTCAGACGAGGATAGAGT
GGGAGGCACGACAGAGCTTGGGACACAGGTATGGAGAGGGGGTTACGGAGGCTAGAGAGGCG
AGACTTACAGGGTCCGGCGGTGGTGAAGATCAGGAGGAGGAGGCCAAACAGAAAGAGGGGAC
AGACGGGCGCACTTGTGGGTTGACAGGCCCTCAGCCATGTGTTGGGAGCCAAGCCACATGGC
FACCAAGTCCCCTACACAGTCCCGGGGCTGCCCTTGGTTCTGTGGTCTTCTGGCCCTGGGGGCC
GGGTGGGCCCCAGGAGGGGTGAGAGCCGCTCCTGTGGAGGGGAGTGCCTGGTGGTCTGTGA
GCCTGGCCGAGCTGCTGACGGGGGGCCGGGGAGCAGCCCTGGGAGAGGACCCCTGGGC
GAGTGGCAATTGCTGCGGTCCGAAGCCACCCATTAGCCAGCAGAGGGGAACCCCGCAATGGC
ACCACTGGGGCCATCTACTTCGACAGGCTCGGTGAACCGAGGGGGTGGCTTTGACGGGCT
CTCTGGCTCCTTGTAGGCCCTGTCCGGGGTGTCTACAGCTCCGGTTCATTGTGTGAAGG
TGTAACAACCGCAAACCTCTCAGGTGAGCTGATGCTGAACAGCTGGCTGTCACTCAGCC
TTTGCAATTGATCCTGACGTGACCGGAGGCGCCACCAAGCTCTGTGCTACTGCCCTTGA
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAAATCTACTGGGTGTTGGAAATAC
CAAGTTCTCTGACTTCTCATCTTCCCTCTCTGAGGAGCAACAACTTTCAAGCACAAGAAT
CCAGCCCCTGACAATTTCTCTTGCCCTCTCTTGCCCAACCAACAGCAGGACGAGAGAG
ACTCCCTTGGCTCCTATCCCACTCTTTGCATGGGACCTGTGCCAAACACCCAAGTTTAA
GAGAAGAGTAGAGCTGTGGCATCTTCAGACCCAGGCCTTTCCACCCACCCACCCCAAGTTACC
CTCCAGCCAGCTGCTGCATCTGTTCTGCTGCTCAGCCCTAGATAGAGGAAGGTGTGGCA
AGAAGGAAGATCTGCATCTACTTTGCGGCCCTGTGCTCTCCGTTCCCCACCACCGCTTCTCT
GCTCAATGCTGATCAGGGACAGGTGGGGCAGGTGAGCTGACGAGGCCCCCAGCAGGAGCCCA
ATGGACAAGCCTCAGCTTACCCTGACGGCTTCTTCTGTGAGGAAGGCCAGCATACGGATC
TCAGCCAGCAGCCTGAGAAGCTGAGCGCAGCAGCTATGGGCTAGGTTGGAGGCTCAGCCA
AGGCAAGAAGGTGGGAAGGGCTGAGATTGTGTGCTGTGAGGAAGGAAGAGGTTATTATG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGGATAGCAATCCT
GGGTGTCTCTTGTATCTGGATCCGAGATGAGCTTGAGCTTGCCCTTACCTCCCACCTGAGATT
GGTGAGTGTGTTTGTCTTGCTTGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATGAAGAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAATCTGCTCCAC
CTTTGAAGTTGAATCTTGAATCCCTCCACACTGACTGCTGCTCTCCTCCAGGCTCTC
TCACTGAGTTATCTTCACTGTACCTGTCCAGCATATCCCACTATCTCTCTCTTCTCTGTAT
CTGTGCTGTCTTATCTCTCTCTTAGGCTTCTTATTACCTGGGATTCATGATTATTCTCCT
CAGACGCTCTCTGCAGTATGCTAAACCTCCTCTCTCTTTCTTATCCGCTGTGCCATT
GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCAGTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTTGAGGTGGATCGGGGTGTACAGGTACAAGTAGGTA
TGTTGACGAGGAAAAAATAATCAAACTGTATCTAAATTAATAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECVVCEPGRAAAGGPGBA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWVPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

[illegible]

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGRWVQKKFQKYIGFA
PCIFHGRGLEFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVGLVINQVQLCTLALWPVSKQLYRRLNCRSLWSQLV
MLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFVGLSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSSLGILYGKK
YEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGVGAASFGVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTGCTTTAGCACTGGGGCACTTCTT
 GCTATTCTTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTAGAAGGGAAGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATGT
 ACATGTGGTGTCTCTTGTGCTTCTCT**GTA**ATGTGGTATGCCATGGGGTCTTGCACAAGCCCT
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAATGCTCTCATAAGACCATTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCAGAATGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTTGTAATTCACACGTTGACTGTGCTTGTGAATTAATCTGGGGA
 TGCAGGTCCTGATTAGTAGGCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACCTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGTTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAAACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCAGATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYTINGDSWGLRPASSVKFLGSAYTFFSLTWHITLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAAC TGCTAGGATTCTGACT **ATGCT**GTGGTGGCTAGTGCTCCTACTCTACCTAC
 ATTAAATCTGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGCCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCAGCTCTGGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGGTGGGCCCTTGCCCTGGCCGTAGAAGGGATT**TGACA**AGCCCGAAGATT
 CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AATCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCACTTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAGGAAC TTGTGCCAAATTATGGGTGAGAAAGATGGAGGTGTTGGGTATACAAAGGC
 ATCAGTCTCTCTGCATTGAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCCATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCCTCTTCCCTC
 TGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCGGGGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG
 GCCACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAAATAAAAAAGAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCCGCGAGTCCGAGACCTGTCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCCTCCTGCCCGCGCC**CATG**ACCCAGCCGGTGCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCCTTCGCCACTGGCTCTTCTTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCGTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTCGAAAATAAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQFPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPGQDSMMTCEQAQLLANLARLIQAKKALDLGTFGTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAGMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGGKPNKRKGFNEGLWEIQNNPHASYSA PPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSDDQDFTPEKKA AVRAPRRGRLGGRKKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSTEPARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAAEVYTRLKSRVLGPKEAV
QKVNKAGMEKEKAEELAGEELAGEEAPQEKAEDKPSDLDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

[illegible]

FIGURE 176

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQTLLLLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDI I FKL DTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTH DHYIRT DISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFFFRSSQEGSTSDKTI LSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSS I FKGSAVCVYSMADIRAVENG P
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINV D YRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTY GKACADCLARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPFDERIIKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACATGAGCTGGAAGCCGAGAGGTCATCTGAGAGCATGCCACCCGCGGGAGCAGA
CAACCTCCCAGTAAAGCTGGGAGCAAGAGCTGAAGCTGTATTTCTCAGGAGCGTGGTGTATTTCCCCACCCCCAC
TCTCAGCAGTTTTCAGCCAGCAGAGGCTGATCAGGTGTGTCTGCTGGAGTGGGAGCAGAAAGCGTGGCTGCGAAGA
GTGGCTTGGAAGAAAGGGTTGACGCTTGACCAGCCGAGCTGCCCGTGAATACAGAGTCCAGAACCATGGGATC
GGGTGAGGTGGGAGGGGACAGGTGTCATGTGCACCTTTCTGTCTCAGCAAGAAAGCTGAGAGAGGGGATCTTTGG
AGCCATTGAGGGGTGTCATGGAGCTCAGAGGGGAGGAAAGGTATTTAAGGTAAAGCTGTGGCACATAAGTTAA
GAGCAGAGTTTGTGGAGCTAGACCACATAGGTTCAAATTTCTCTGTGCTTCTAGTTCTGTAGCCCCAGGT
AAGGAGGTGACTTAACTCTCTGGACTTCAATTTCTCTCATCTAAAGTAGGGCCAAATAAGTACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGATGCACTAGCAAAAGTACCACTCCCATAGTAAGTCACTGCCCCACAG
TATTTCCACCCACCCCTGTCTCTGCCCTCCCAACAGGTAAGTGCACAGCACTGGAGCAGAGGGCGGAGCAGGCTT
CAGAGCGGAGGCTCCAAGCATAGAAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGACAGGTGAGCC
AGGTGAAGGGGGCTGCCGCTGGCCCTGTCTGACGGGGGCTGGCTTAGATGTGAGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGCTCAGTGAGGCTCGGCTGTCCCAGAGGACCTCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCCAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAACTACGAGGGGTGAGTGGCTGGAGGTGATAGAGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACGAGCACGGCAGGTAGGCTTTGTCCCTGAGCATACTCAACTTCCCGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAACTCCCTCGGGGACAGCCACAGCATCTCTGGCAGAGCCCTGTACAGCTACACCCGAGACA
GTGCAGAGAGCTGAGCTTCCCTGAGGGGCACTCATCCGTGCTGCCCGGCAAGATGAGTAGATGAAG
GCTTCTGAGAGGGGAATTTGGGGGCGGTGTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTTGTGGCCCCC
CAGGGCCAGCTGAACCTCTGACCTTGACAGATGCTGCCCTCCCTCTCTCCAGCTTCTCCCACTGCAC
CTACCTCTGTGTGGATGGGCCCCCTGCACCTGTCTGCTGCCGGGACAAAGCCCTGGACTTCCCTGGGTTCTGG
ACATGATGGCAGCTGACTCAGGCCGATGCGTCCACCACTCTCCCGCCGCTAAAGCCCGGATCTGGCCACC
CAGATCCCTCACCCTGAGGCGCAGGGAAGCCTTGACCCCGCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTCCAGA
CCACACCATCAATGATCCAGAGCAACAGCCAAAGCTGGAATCGCCCTTATTTCTACCTCTACCTTCAAGGGT
GGAAAGCTGCCCTTCCCAATTTCTAGAGCTGGAACCCACTCTTTTCTTCTTCTTCTATCATCTCTAGGAC
GGAACTACTACCTTCTCTCTGATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGTGGAAAC
ATCCATCAAGGTCTTAGTAGTTTGGCCCACTCTTCCCACTCGGCTCCATGACCCAGCCCACTCTGGATG
CCAGGGTCACTGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATCGGAAGCAG
CTGTAATGGTCTGAGCGGATTATTGACAACTGAATAAGGGCACGAGGGCCAGGCCAGGGCTGGGCTCTTTGT
CTAAGAGGGCAGGGGCTACGGTGCTATTGCTTTAGGGGCCACACCGGGCAGGGGCTGCTCCAGCTGCCAC
GCTCTATCATATGGAGCAGGTGTTGGGGAAGCGGGGAGGAGCTGTTGACGGCAGGGGAAGGAGAAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGTGCCCT
AGCTGGGGGCAAGTGTCTCCAGTGGAGGGGAGGGCTTTCACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTCTCAAGCTGTGTCCAG
TTTTCCCTCGGGCTCAGGACCTTCCCTACCTCCACCAACCAAGGGATTATAGCAAGCTGAAGCTGC
AGTTTACTCTGGGGTTCAGGAGCGGCAAGGCTTAATAGTTTAAGTAGTGATGGGAAGATGAGATTACCTCA
TTTAGGCTCAGGCAGCACTCACTCACATACTCCCTGCTCCCTGTGTAGAGACACTGAGAGAAAGGGGAGGG
TCAACAAATGAGAGCAGGAGGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGCTGG
AGTCCCGCTGTGTTTCTTACCTGTTGATCAGAAAGTGTCTGGTTGCTTGGCTGCCATTGGCTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTGTGCAAGAGCTTGGGTTCCCTTCAAGT
CAGCAGGGTTAGGCTGTGCTGCCGTGACTCTCCATTCTGTACTGGGGAGCTGCTGAGGCTGGGGCTGTGGCC
TCTCAGGGGACGCTCTCCATGGCAGGATCCCTGCTTGGGCTGCCCTCCCGAGACCTGACACCCCTGCT
GGCTGTGCCCCACAGAGCCAGCTCTGTCTGTGGGAGAGCACTCAGGCTTGTCTGTGAGTCCATAGGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGTTTAGGACCAAACTCAGAGGGTGTGTT
GCCCTCCCTCTGACCCAGGACATCTGAGTTTGGTGGCTACTTTCAGCTAGGAGAGGGGCTCTC
AGATTGTGGGGCAATGTGTAGCTGACTTCTGTGAGCTCCAGTCCAGGAGGAAGAGCCAGGGCCACTT
TTGGGATCAGGTGCTGATCATCTGGGCCCTTACCTAGCCCCCTTTCCTGGAGCACTGCTCCCACTGCCCA
CAGAGAGCTAGCTGGTCTCCCTCTCGGGGGCGGCTTTTCTCTCTTGGAGCTGCTGCTGACGGCAAGTGGAG
GGCTTGTCTGCGGCTGCAATGGATGCAAGGGGCTGACAGCCAGGTGCTGATGATGAGGGAGGGGCT
CGTCCCTGAGGCTGGAGTGGCATCCACTGGACAGGAGGAGGGAGTGGGGTAACTTTCCATTTCCCT
TCTAGTTTGTGTTTCTTACGTTCTTCTTACGATGCTCTTAAACCCGAGAGCCCAATTTCCCCAAGCCCCATT

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDAEIS
DFEECEETGELFEEPAQALATRALPCPAHVVFVFRYQAGREDELTITEGEWLEWIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPSSQSDNPGCAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSLVDGPPAPVLPFGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDLT
```

CACGGAGGACCCACAGACATATGACGAGGACAGACAGGAGGAAGACAGACAGACAAAGGCCACGGCGGAA
 GAGGACGAGACAGCGGAGGACGAGCATAGGAGCGGCCAGAGACAGTCTCCACAGGAGGAGGCCACAGAGAGCTGACG
 AGACACAGGACGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGAGAGATTTGGAGACGCCACAGCCCTGG
 GCACCTCTCTCCAAAGCCCAAGGACTAAGTTTTCATTCTCTTTACAGCTGCTCAGCCCTCTTGAAATCTTGCC
 TGTGACCTTTGGCAGGATCCAAAGCCCCAGGCTACAGAGAGAGACTTTCCAAAGCTAGGCTGTGGAGAGACTTGT
 CCGCTAGACGGCTCAGTCTGCTCTCCAGCTCAGTACAGTGCACATGACAGACAGTCCGATCCCGGAGGGGG
 CTTGCGACGGGCGTCTGCTCTGCGGAGCCCAACCTCTGCCCTCTGCTCCCATTGTGCGCTCTCTGCTGGCTGGTGTG
 GCTGCTCTCTGCTACTGCTGGCTCTCTCTGCCCTCAGCCCGGCTGGCCAGGCCCTCCCCTGGGAGGAGGAGAT
 CGTGTCTTCCAGAGAAAGCTCAACGCGAGCTCTCTGCTGGCTCGGGCGCCCTCGCAGGCTGTGTGGCGCTTGG
 GCGCTTTGGGAGACGCTCTGACTAGAGCTTGAGACAGGATCTCGGCTGTGCAGCTTCAGGAGGCTGACGTCGAGT
 CTGCGCCACAGGCGCTGAGCTCTGGTGGTGAGACAGGCTCGACCTGCTGAGCTGACGACCATCAATGGAGTGA
 GAGTCTGGTGGCATCTCTGACCTGGGATGGGGAGCGCTGTAGGCGTGTACAATCTCGGGGGCTGAACTCCA
 CTCCAGCCCTCGGAGGGGAGCCCACTAACTCTCTGGGGAGCTGGGGCTCATCTCTACGCGGAGAGAGTCC
 CTGACGGGCTCAAGTCCGATGTGCACTCAAGGCTCTCTTGGAAGCCAGCCGCCACACCGGAGAGGCGAA
 GCGCTTTGCTTCATGAGTAGATTTTGTGGAGACATGTGTGGTCAGATGACAGATGGCCGATTCACAGGTCG
 GGGGCTAAAGCGCTACTCTGTAACAAGTAGTGACACAGGCGCAAGCCTCTCAAGACCAAGGATCTCCGAATCC
 TGTCACTTGTGGTGATCTCGGTAAGTATCTCGGCTGAGGCGAGGGGGCCCAAGTGGGGCGGACGTGCTGC
 CAGACCTCTCGCAGCTCTCTGCTGGCAGCGGGGCTCAACACCTTAGGACTCGGGCGCTGACCACTTCACTT
 CACAGCCATTCTGTTTACCCTCAGGACCTGTGTGGATCTCACTTGCACAGCTGGGATGTGCTGATGTGGG
 CACCGTCTCATGCGCGGCTCGAGGCTCTGCCATTGTGGAGGATGATGGGCTCAGTCAAGCTTCACTGCTGTCA
 TGAATGGGTCTGCTCTCAACATGCTCAATCAACAATCAAGCATGATCACTTGAATGGGCTTTAGACAC
 CTCTCGCATGCTTGTGGAGCTGTGATGTGGCTCATGTGATCTCGAGGAGCCCTGGTCCCCCTGAGTGCGCCGT
 CATCACTGACTCTTGGCACAATGCTATGGGCACTGTCTCTAGACAAACAGAGGCTCAATGATCTGCTGTT
 GACTTTCCTTGCAAGGACTATGATCTGACCGCAGTCCGAGCTGACTTTCGGGCGGCACTCAGCCATGTGTCC
 ACAGCTCGCCCGCGCTGTGCTGCCCTCTGGTGCTCTGGCCACTCAATGGCATGCCATGTGCGACACAAACA
 CTCTGCCCTGGGCGGATGGACACCTCGCGGGCCGACAGGCTCGATGGGTGTGCTGCTGCTCCACATGTGACCA
 GCTCAGGACTCAATATTCACAGGCTGTGGTGGCTCTGGGACATCTGGGAGTACTGCTCTCGAGCTCT
 TGGGGTGGTGTGCACTCTCTCTCGAGAGTACGACAGGCTGTCCCCCGAATGGTGCAAGTACTGTGAGGG
 CGCGGATACCGGCTTCGCTCTCTCAACACTGAGGACTGCCCACTGGCTCAGCTGACTTTCGCGAGGAGCA
 GTGTGCTGCTCAACACCCAGCCAGCAGCTCTCTCAAGAGCTTCCAGGGCCCTGAGTGGGTCTCTGCTCAAC
 AGGCTGGGCCGCCCGGACAGGACCTGCAAACTCACTCGACGCGGGGCACTGGGTACTACTATGCTGTGGAGC
 ACGGTTGGATGATGGGACCCCTGTCCCCGAGACGCTCTCGGCTCTGTCTCAGGCGGATGCATCATCTGTGG
 GTGTGATGAGCATTTGGTCCACAGAAGAATTCAGCAAGTACAGTGTGCGAGGGGACGGTTCTGTTGACG
 CAAAGCATCAGGCTCTCAGGAATCTGAGTACGGATACAACATTTGGTCACTATCCCCGGGGGCGACCCA
 CATTTCTGTGCGGCACAGGAAACCTCGGCACCGAGCACTACTTGGGCTGAAGCTGCCAGTGGCTCGAT
 TGCCCTCAATGGTCAATACGCTCTGCTCCCTCCCCACAGTGTGGTACTGCTGGGCGAGTCAGCTTGCCTA
 CAGCGGGCGGCTGACGCTCAGACACTGTCAGCGCACTGGGCGACTGGCCAGCTCTTGACACTCAGCTCG
 AGTGGCTGGACACCCCGGACAGCAAGCTCCGATCAGACTCTCTGCTGGCCCGGCGACCGCTCAACAGCCAC
 CCGCTCTCCGCCAGCTGCTGCGACCGAGGACAGATCTGGAGATCTCTCGGCGCGCCCTCGGCGGGGCGG
 GAAA**TAA**CTCACTACTCGGCTGCCCTTTCTGGGACCGGGGCTCGGACTAGCTGGGAGGAAGAGAGCGGAT
 CTGCTGCTGCTCATGCTAAGACTCAGTGGGAGGAGCTTGGGCGTGAGACTGCCCTCTCTCTGCCCTAAT
 GCGAGGCTGGCCCTGCCCTGGTTCTCTCGCTGGGAGGCGATGTGGGTTAGTGGAATGAAGGGGCTGACAG
 AGCCTCCCATCTAACTGCCCTCTGCCCTCGGCTCACAGGAGGGGGGGAAGCAGGAGGGGCTGGGGCC
 CAGTTGATTTATTAGTATTTATTCACTTTTATTAGCACAGGAGAGGGGACAAGACTAGGCTCTGGGGAA
 CCGTACCCCTGACCCCTCATAGCCTCACCCCTGGGGCTAGGAATCCAGGGTGGTGGTGAATAGGTATAGTGGTG
 TGTGATCGGTGTGTGTGTGTGTGTAAGATTTGTGTGTCTATGATGAGGTACAACCTGTTCTGCTTCTCT
 TCTCGAATTTATTTTTGGGAAAGAAAAGTCAAGGTTAGGGTGGGCCCTCAGGAGTAGGAGTATCTTTT
 TTTTCTTTCTTTCTTTCTTTCTTTTGTGGACAGAACTCGCTCTGTGCCCGAGCTGGAGTGCATG
 GCACATCTCGGCTCACTGATCTCGGCTCGCGGGTCAAGTGAATCTCAGTACCTCAGCTCTCTGCTCAGCTCT
 GGAATTACAGCTCTCGGCACAGCGCCAGCTAATTTTGTGTTGTGGAGACAGAGTCTGCGTATTTGTC
 ACAGGCTGGATGATTTCACTCATCTGCTCAACTCTCGGCACCTGGGTCACAGATCTCTGCTCCTCAGCTCT
 CAGGTAGTCAAGTCAATAGGACACCTACCAACGCCCGGCTAATTTGTATTTAGTAGAGACGGGTTTCAAC
 CATGTTGGCCAGCTGCTGCTGCAACTCTGACCTTAGGTAGTACACTCGCTCATCTCCAAAGTCTGGGAT
 ACAGGCTGAGCACCGCTGCTGGCAGCCGCCAATCAATTTGTATTTTAGTAGAGACAGGTTTCAACATGT
 TGGCAGGCTGCTCTGAACTCTGACCTCAGGATCAATCGACTGCTCGGCTCCAAAGTCTGGGATACAGG
 TGTGAGCCAGCACCGCCGCTACATATTTTAAATGAACTCTACTATTTATGTATCTTTGGAGTCAGACAC

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCCTCGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTCTGAGGATTAAATAATGTAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLPSARLASPLPREEEIV
 FEKLNQSVLPFGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLQGAPELIGGAEP
 GTYLTGTINGDPESVASLHWDGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
 ASGQGPNCNVKAPLGSPSPRRRAKRFAASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGSPSAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPKDYDADRQCQLTFGPDSSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCCLHMDQLQDFNIPOAGGWGPWGPWGDCSRCTCGGQVQFSSRDCTRPVPRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRDTLFSKSPGPMWDVVPYRTGVAPQDQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHRSIYLAKLPDGSYALNGEYTL
 MPSPTDDVLPGAVSLRYSGATAASETLSGHGGLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRETPQDWLHRRQAILEILRRFPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAGT
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTATTGTTGTATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TAAT**AGGAGTTTGAGCTCAATGCCTTAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSSELQDFEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEFDPMLDERGYCCICYCRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCAATGGGCCAGCAGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCAGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGGCGCACCCCTCTTCATCCTGGCGGCCCTCCTGTGCATGGTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCTGCTTTGCCCTGTCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAAAACACGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
 TGAAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAÀAATCCTGTCTGTTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAFSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

bioRxiv preprint doi: <https://doi.org/10.1101/2021.01.11.424444>; this version posted January 11, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

FIGURE 185

GAGTCCCCCTCAGGAGCGCGTTAGCTTCACACTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT
CCTGTCCATCCTGGGGCTGGCGGCTGCATCGCGCCACC GGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTACC GAATGCAAGGCCCTATTTCACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
STCTGTGTTTGCCAACATGCTGGTGACTAACTCTTGAGTGTTCCAGCTAACATGTACACCG
CATGGTGGTGGGATGGTGACAGTGTTCACAGCAGGTACACATTTGGTGGCGCTCTGTTCTGT
GGCTGGGTGCTGTGGAGGCTCACATAATTGGGGGTGTGATGATGTGCATCGCCTCGCCGGGG
CCTGGCACCAAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCTCAGGCCACAGTGTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGCACTA
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAA
AACAAAGGAGATCCCATCTAGATTCTTCTTGTCTTTGACTCAGAGCTGGAAGTTAGAAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATCC
ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTAGTATCTCCCCACCCCACTTTGGCTAGTATAAAACCTTACTGAGAA
GAAGCAATTAGAGAAAGATATTGTGAATCTCTCAGCCCATGATCTCGGTTCTTCTACACTG
TGATCTTAAAGTTACCAACCAAAAGTCATTTTCAGTTTGGGCAACCAAAACCTTCTACTG
CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGGTGAGAAATGTCCCTAGATGAATGAGAAAAATTATTTTTTTTAAAT
TTAAGTCTTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAAGGTTCCAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
AGGTTGGGGCTGACAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCTGCTGTAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
ACTAATCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GCGTGTCTTCTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCAATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCATCGCACACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAATCTATACTTTCTCAAATGGACCCAAAGAACTTTGATTATA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGCTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTACGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGTGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACTTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAATAATGAAGGCTTTAATCAGCATTGTAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCTTGTTGATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTGTGATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGCTTTGGTTTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTGACCATTTCTGTTTAGTTTTACTAA
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTTGTGTCGAGCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA
 TTAATAAATTGTACATTTTTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCCATGGCCTCTGCCGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGC AAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCTATCGCCCTCCTTGTGGCCCTGTTCCGGCTTGCTGGTCTACCTTGCTGGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCAACCTCTGGGA
 TTGTCTTTGTCTCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT
 CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTGTGTGTGTGCACTT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
 CGTACCTTTTGTCTGCTCCTGCTATTTTCTTTTGACTGAGGATATTTAAATTCATTT
 GAAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTAGGCTCTGCTGTTTCTACCCCTTGG
 ATGATGGAGCCAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
 CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCCCAAGAGTTCTGTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCATCCTACTCAGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTTGACCTCTGTTTCTCCGTCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACACTCACATTTTATCAAATAAAGCATG
 TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGLGWAASGLLLGGGLLCCTCP
SGGSQGPHYMARYSTSAPAIRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCAGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCACTTCAAAGTAAAGGCAATGGCATTATATCCC
TTGCAAAATGCTGGGCTGGTCTTGGGTTCCTTGGCATGGTGGGACTCTTGCCACAACCTT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTTGGCAGCAACATTATGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGAATAGAAATGCATCCGACAAGCCAGGGTCCGGTTCGAATGCAAGTTCTA
TAGTCTCTTGTGGCTCTCCCGCTGCGCTGGAAACAGCCCAGGCTTCTATGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGACA
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTTCATCCTGAC
GGGTATCTTCGTTCTGATTCGGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCTTGCTGGGCA
AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAGTCTTGCTAGAAATGTAAGTATGTGAGGCAGGA
GAACCTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCAAATTCAGTATACCATTAATCATATTGCAAG
TGTACAATCGTGACTACTTATTACTTTTGGACATCATGTATATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRNTTMLSKTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACATTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACAGTCAATAAAAAAATAATCTCCAGA

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSSEASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATGG**GCTGCCTCCCCCGCGCGGCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAATAGCGATTC
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTACAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD
EDSAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCTTGATTGAAGGGGTGGGTGATGAGGTGAC
 CGTCTTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCAGCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCGAGGGGCAGAGACCCCGAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTACAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCAGACCCTGG
 GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAATCCCCCTGCCCCGCGGGTCCGAGCCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCTGCTGCTCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CTTCTTTTCCCTGACCGCCACTCTGGGCTTGCCGGCTTACCCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCCCTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCGCCGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
 CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGACTGCGGAGG
 CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCGCTGCCTCGGCCCGGGCAGAGCCG
 GGCCGCCCGGGGGCCGCTTTAGTGTTCTGCCGAGGACCCAGCCGCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGAG
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPFPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATTGGGTTTGAGGGTTACTCCCTGAGTGACTGCTGTGCCTTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAGATAAATGAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCAGATCAACAGCCACTACTGGTGAACAGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCAGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGACCCGTGG
AGTCATTCCAAGACTCCTGTCTCTACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATTGTATTTTCTTCCCTTCCATTTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
TTGGTTTTCTGGTCTCCTCTTACTCCCATCCCATCTGGACCCAGTCCCTGGTTCTGTCTGTTAT
TTGTAACCTGAGGACCACAATAAGAAATCTTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

100673-120601

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATTATACAAAGGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTTATTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCTACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC
 TGTGTGGCAAATGTGAGACCAGGTTAAGTGACTGGCAGAAAACTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAATTGAACATGAC
 CTGTTGCATTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCTGCAACAGACTGTCACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTGGACTTTGGGGAAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGCCAGAAAGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGAGCCTGGACCCAC
 GTGGCCTCCAGGAGGCATCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCCG
 CACCCACTGTGTCTGCAGCAGCCCTCAGGACAGCCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGCAACTCAAG
 TCTGCTCTCAGCAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGAACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGGACTGGAAGCTGGATTTCCTACTGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAAGCTGTCTTCAAGGCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGCTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACAGTGC AAAGGAGACTGGGTGTGTCGGACATTCACATG
 TTTCTGGCTAATGTCTACCTCGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACTGTCAGCACACCAGC
 AGGAAGGAGATTCACTTTGGCAGGCCACAGCACTGTGCTTGTGTCAGGCAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCGTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGAAGAAAAAC
 AATAAGATTGTGACTGCGTCCGTGTGATGGAAGAGCCCGCAGCAGTGGCGATTGGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGCAAGAAGGAAAAGAAATTTGGCCATC
 AAAATCCAGCTCAAAGTGAAGCTAAGAGCTTATATTTTCAATGAGCTGATCCTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTQAASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVS
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDSHSPLDQEATL
RNRVRIAETWLGSKFETFYKHSPEAFSLSKAEKPCMERLQLQRRLCRTFWHFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYQLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWDFFQENGMIHVHILSGKCMEEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCTCCCAACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAAACCCACAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCACGTCTGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCTGCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGGCCCTCATCCCCAATACCCCTGGGCT
 ATCGTGTGGGCTCCACCGTGTCTCAGAGGATGGAGGGGACCCCACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTCTTTCAGCCCTCATGGCTCGCAACCCACACCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGACCTGCCACCCCTGCGGCCATT
 CTGTTCTGGGGGCGTGGGGAAGGTGTGGACCCCAAGCTCTATGTACAATTACCATTCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGCCCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGTTCAGGGCAGGGGCAATGGATGGGAGGGAAGAGGGAAGGCAAC
 TTAGTCTTCAGGCTGGGTGGGGTGCCCTTGATGGTAGTGAGGAGGCAAGGATGCTGGC
 CTCCACAGCCCTGCCCCCTCCCAAGGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTCTCATGCCACCTTGCTAAGACAACCTCGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCTTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCAATGTTGGGGTGACGC
 AAGCAGGAGGGCAAGGGGCGGCACAGCCCCATCCCACTGAGGCTGGGGCAGCTGTGGGGA
 GCTGGGGCAACAGGGGCTCCTGGCTCCTGCCCTTGACACCAACCCGGAACACTCCCCAGCC
 CCACGGCAACTATCTGCTCGCCCTCCTGCAGGTGGGGCTCACAATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACTACCTCCACCTTCAC
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCTCCACATTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCCTCG
 GTGCTGCTCCAGAGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTGATGG
 TCTGTCCTCATCCACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTACCCCCAGCCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTTGGGAGTCGCTGCACTACATGAGAA
 AGGACTCCCATTTGCCCTTCCTTTCTCCTACAGTCCCTTTGTCTGTGCTGCTGGCTG
 TCTGTGTGTGGCCATCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTCCAGCCT
 CCTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCAGTGGTTCAGAGCTT
 ATCGGAGCTCTGCCTCCAAGTCTACCCCTTCCCTTCCCGACTCCCTCTGCTCCCTCTCTT
 CTTCCCTCCTCTCTCCTCTCCCTCTCCTTTGCTTCCCTGCCCTTCCCTCCCTCCTCAGGTT
 CTTCCTCTCTCACTGGTTTTTCCACCTTCTCCTTCCCTCTCTCCCTGGCTCCTAGGCT
 GTGATATATTTTTGTATTATCTCTTCTTCTTCTGTGGTGATCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTCAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGFAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWSVSRIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGGATG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCTTGGTGTGCTTACAGCGCGCGCTGGCCCA
CGGCTGTCTGCACATGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCTCTGGTGGGTGGGCGACATCCCCGTGTCAAGGGCGCTGCTCACCAGCTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACAGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC
CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGCAT
CGACTGTACGACCCGTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCAGCTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCTTGGAGGGGCTCCCCGCTTCCAC
CTGGCTGTATCGGGTAGGGCGGGCCGTGGGTTTCAAGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
TGGCACAAGTAAGTCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGCGGCTGCAGTCTTTTCTCCCTCAAAG
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCATAGGGTCTGGTTCC
ACCCCATCCAGGTCGTGTGTGAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACCCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACAGCGTGCCGCGGCCTGCACACCTTCGGACATCCAGGC
ACGAGGGTGTCTGATGTGGCCACACATAGGACCAACGTCACGCTGGGAGGAGAGGCCT
GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCGCGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
```

```
><subunit 1 of 1, 157 aa, 1 stop
```

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAGCLHCHSNFSKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMSPSPRGDLF

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**AATG**GAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTCTC
 CCTCACGTGTGAGCTGGCTGCAGAAAGTTGCTGCAGAAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCATTTGGGATCAGCACTGATTTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTTAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTGAGATTCTCTCTCTGATAATGAACAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATTTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTGA**CTTCTCCTTGAACTACATATGGCC
 AAGTATCTACTTTATGCAAGTAAAAAGGCACAACCTCAAATCTCAGAGACATAAACACAG
 GATCACTAGGCCTGCCAACCAACACACACACGCGTGCACACACGACGACGCGGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCTCTTTTAAATTTATATCCTCACTCCCTATCCAATTTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTTGCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGGC**CAGCGTCCGCCGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGCGCTGGCTGTGGTTCGGTGTGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGATTTGTACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCACTCATATATGCACAGTTAGACCACTCCGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
AGCCTTGGAGACCCAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGTCATGA
TGAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGTGTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGCTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAGGATAAATCCCGAAG
GTCACTTCAATCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
GAGAACTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTA

FIGURE 212

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGTCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGT CAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCGCGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCGGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGACAGCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGT CACAACAAGATTACTGATTTCCCATTTAAGTGGAAATCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAGAGAAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTAAAAATTC AATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTGTATTCA
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCRRGVHQHAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCPKPTVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGCGCGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACCTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCAGGAGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTTCGACCCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCGAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCGAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCCTCCCTGTAAAGTCTATTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGTCACTTGATACGTTATTTCAGAAACCCAAG
 GAATGGCTGTCCCATCTCATGTGGCTGTGTGGAGCTCAGTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPIRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGAGCAGGTCTCCGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGTCTTTGTAGGCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCTTCGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTAATACTTCTTGGAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGTCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCTATCTTTGTCTTCTT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGCTGCTCATCGTCTCTTCTCTCTTCTATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCTTAGGGCT
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACGCACTTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTTCTCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSTRCAGGLRCLLSDRR
 VLLGLTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIIVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVIPET
 EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCGGGCCGGGCCCTGGAG**ATG**
 GTCCCGGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGGT**TAGA**AGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTGTAGCAATAAA
 GCTTCTCATCAGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
 ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACCTGCGGACTAGGTGGCAG
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
 TTATCTCAACGCTATTGTTTAAATGGCTGTGTTTAAATGTGATCTATCTGGAAAATGAGGACTC
 CGAATAAAAAGCTATTACTAWTNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPHYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQCGGIYKDNNKSSIHCMDSLQRYCLMAVFNVIYLENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**GATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATA
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCACTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSPPVGR
```

Signal peptide:

amino acids 1-22

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAGAATTTGTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTTCTCTGGAGTGTTCTGCGTGGCTGGCAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCCGACTACACGTGACGTG
 ACAGGGGCTCTCATGCAACTGCCCCATAAGCCAAGCAAAAGACCTTAAGGACGACCTTTGAA
 CAATACAAAGGATCGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAATGCTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCCAAAATGGTATATTGTGAATCTCAGAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACGAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGAGACTCAAAGAGCTGATTCTTAGTTCCAAATAGAA
 TCTCTTATTTTCTTAACATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTTCTTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGGAAGTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACCTTCACTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCGGAATCTGCAGCGCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGCGAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCTGTGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGACGACGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCGAGCACCGAATTTTATGTAGATTATAAACCCCAACACGAGACCGAGCGGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAGAGCTCTTAAAGCTGGGAAATAAAGTGGTCTTATTGAACCT
 TGGTGACTATCAAGGGAAACGGATGCCCCCCCTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTTGTGCGTTTTAGTGCATTCTAATACTGGTCATTTCTCTCATACATA
 ATCAACCCATTGAATTTAAATACCAACATCAATGTGAAGCTTGAACCTCCGGTTTAATATA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAAGTATGTCGATTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGC PKGRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNL YLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQE FYVDYKPTNTETSEMLLN
GTGPGCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

- amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTCGCGCTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTCTGCTCCATGTTTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTTGA
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTCAAGTTGTTGGAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAATAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTATTGCGACATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRPRIDSHRRTMVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGACGCTGACGCCCGCTTATTA
 GCTCTCGCTCGCTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGCGACCCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTCTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTAAACT
 CCCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTGTCTCTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGACAATT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAAGAACGAATGCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATTCGTACATATAAAATTTTAAAGTTATTGTTTGGCTTCAGGCAAGTCTGTTCAATG
 CTGTACTATTGCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTAATATATTTTGTATTCCAATTATGAGCAGAGAAAGGAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATACTGA
 AGTTAATTTGTATATTTTAAAAATTACACTATAAGAGTATAATCTTGAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGGATTAATAAGTT
 GTAAACTCTAATCTTATACTTATGAAGAATAAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTCATACATACATGAATGTTTCAATTTAAAGTTAATGCTTTGAGTGTCT
 ATGCTATCAGGAAGCACATTATTTCCATATTGGGTAAATTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGATATATAATAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGAAAAGTGTTAAACATTATATTATATAAGAGTATC
 CTTTATGAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAAAGAACATTTAAAAATATAAACCCTATGAAGATTGACATCTTTTCAGGAAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTTGGGTAATTTCTAGTATAAAACAAATTACTTTTAT
 TTAATTTCCCTTGAGCAAACTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCATAGTAACGTCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAAATTTAGATAT
 TGTATTGTTGCTCATTTATAATATGCTACCACATGTAGCAATAATTAACAATTTTTATTAAAA
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
 CTGCTCACTTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

GCGGCGCGGGCCGCCCGGGTGAGCTGTCCGAGGCGGCTGTGGCGCAGGCTTCCAGGCCCCAC
CATGCGGTGGCCCTGCTGCTGCTGTGCCCGTGAGTGGGGCCGAGACAACCCGGCCATGCT
 TCCCGGGTGCCAAATGCGAGGTGGAGACCTTCCGCTTTTCGACAGCTTCAGCCTGACTGCG
 GTGATTTGTAGCGGCCCTGGGCCCCACATCATGCCGTTGCCATCCCTCTGGACACAGCCCA
 CTGGACCTGTCTTCCAACCGGTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGCT
 ACACGACGTGTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGACATCTCACCACCTGCC
 TTCTTCCGCGCTTCTGCTACTCTGAGTGTGCTTTGACCTCAGGCACAATGCCCTGACAGCGCTGCC
 AGCGGAGAGCTTACAGGACTACCCCTGAGCGAGCTGAACCTTAGCCACAACAGCTCCGG
 AGGTCTCAGTGTCTGCTTTCACGACGCACAGTCAGGGCCGGGCACTACAGTGGACCTCTC
 CACAAACCTCATTACCGGCTCTGTGTCACCCACCCACGAGGGCGGGCTGCTTGGCTCGCCACCT
 TCAGAGCTGAACCTGGCTGGCTGACCAACGGCTTCATGCGTGCCAACCTCCGAGACTTGCCT
 TGCGCTACTCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGTCGGGTGCTTTCGCGGG
 CTGGGAGGCTTACACACCTGTCTCTGGCCAGCTCAGAGGCTCCCTGAGCTGGCGCCAC
 TGGCTTCGCTGAGCTACCGGGCTGAGGCTCTGAGCTTGTGGGCAACCCAAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTTTCAGGCTGAGCTCCCTGACGAGCTTGGACCTTCTGGGCA
 AACCTGTGCGCTTCTGCTGAGGCGTGCTCTCCACCTCCCGGCATCTGCAGAGCGTTCAGCT
 GGGCCAGGATGTGCGGTGCCGGCGCTGTGTGGGAGAGGCACTTACCCCGAGGGCTGGCT
 CCAGGCCCAAGGTGCCCTGCATCTGCTAGACACCCGGAATCTGCTTCCAGGGGCCCAAC
 ATCTCT**TGGA**CAAAATGGTGTGGCCCAAGGGCCACATAACAGACTGCTGTCTGGGCTGCCCT
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGAGCCCGCAGGCCATATGTGGCA
 CGCTCACCACAGGAGTGTGGGGCTTAGGAGAGGCTTTGGACCTGGGAGGCAACACCTAGGAG
 AAGGTCTACCCCTTTGTCTAGTTGCTTCCCAAAACATGAGCAGAGGAGCTTCGATGCCA
 AACCAGACTTGGGTCCCCCTGCTGCTTCCCTTCCCATCTGATCCCCCAAGTGCTTCCCTCAT
 GCTGGCGCGGCTGACCCGCAAGTGGGCAGAGGGTGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAAGTCCACTGGGCTGAGTGTCCCTTGGGCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTTCTTAACATAGCCTTTCTTTGCCATTGAGGCACTGAGGCGCGCTTCATCTTCTTATG
 TTCCCTAGAACCTTAATGGTGAAGAAATGCAAAATCAAGTCACCCCTTCTCATGTGAC
 AGATGGGAAACTTAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCTTGCGGCAGTGGC
 ATGACTGGAGCAGACCTCTCTGCTCCAGCGCGGCAACATGCATTTCTTGCTCTCTTA
 ATAAGGCCCAACCTTCCCGCTGGGCTCCCTTGTCTGCTGCTTCCCTATTCACCTTAGACA
 GGATGAGCAGCAGCAGGACAGCAGAGGCTCACAAGTGGGACTTGGGCTCTGACACGACT
 TGTGGCGCTGGCTTAAGTCACTCTGCCCTTCGGAGCTCTGGAAGCTTAGGGCACAATGGT
 CCAGCCTAGCAGTTTCTCACCTTGGGTGGGGTCCCCAGCATCAGACTTGAACCTTACC
 CATTTTCCCTGAGCATCTCTTAGATGCTGCCCAAGGAGTGTCTGCAGTCTGAGAGCTCA
 TTTGGCTGGGATCTCAAGAGGCTTCTGTGATTCAAGTCCCATGCGCTGAGCAGCAGAC
 CCTTCTTACCCTCCAGGAATGCCGTGAAGGAGACAAGGCTTGCCTGACCCCATGTCTATGC
 TCTACCCCTCAGGCGAGCATCTCAGTCTCCGAACCTGGGCTGTTTCTTAGTCTTCATTTTA
 TAAAGATTGTGCTTTTAAACGAGGTGACCTTTCAACCGGCTCCCCTACCTCGCTTGGC
 CGGGGATGAGACATGTTCATTTGTAAAGCAGAAAAGGTGCATTTGCTCATTTTGTAA
 ATTGTCTTGGCTGTGTGGGTGTGGGGAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCTCAGGCGAGTGTGCTGTCTTCCCCCACTGCTGCTAGC
 CCAATCATATCTAACCGGTCTTGATTTAATAAAACATATAAAAGGTTTAAAAAATAAAAA
 AAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLNSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSDGNPKLNWAGAEVFSGLSSLQELDSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGCT
 GTTCCAGGCTTACCTGCTGGGCACTAACGGCGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTAGGCGCTAAGATGAAAGCC
 TCTAGTCTTGCCCTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCGATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGTCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATTTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAGCACTTGTAAATTCAGAAAGAGTGGCT
 AGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNK GATT CATNSHSDSEL RP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSF LTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCGCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCCTTTGGAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAAACCATTGCGATTTTCGTGGTGACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT
 ATTGAATACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATATGAATCAACCA
 CGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTTCAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFSGKSEDEH
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGGKPLRFRGVVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGCGAGGCTTCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTATCCTAAGCCAGAACAGTTGAACCATGCCCTT
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTTACATTTTATGTTT
 TGAGTTTGAATAGTTTATGAAATTCCTTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTATTCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
 AAAAAACAAAAATAGCCAGGCATGGTGGTGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTAGCCTGGGGGAGAAAGTGAACCTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA
 AAAAAATTTTGTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
 AAAGGACTAGTTTGAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCGAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTGAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAGGCCACCCCTTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCTGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACGAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAACAATAACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTCTGTCAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
 TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSFSMKTIRLPWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLKFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCTAGTCTCTAGTCTCAAATTCACAGTCCC
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCCAGTCGCCCATCGATATTGAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCCGAGC
 CTTTGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCATGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTACCTCAGCACAAGCCACGACTGAGGCATTAAATTCTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTATGATCAATA
 TATTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLF
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSDSLSEAAERPQGLAVLGILIEVGETKNIAIEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLL
FSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVGCICLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTAPAGRLPTPSG
TDDDFAVTTTLAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATGC**GACCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATCCGGGTACACCTG
 GGATCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGAAAGCTTTGAG
 GAGTCTTGGACACCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTGAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATTCACAATTAATATTCATCGCACTTCTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCCTTGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTGCTTCAATCAAAGT
 GGTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATGTTGTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAAATTTTTTTTATCTGTTAAAT
 AAAAATATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPENM
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217